

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: April 8, 2004, 15:30:06 ; Search time 43.3077 Seconds  
(without alignments)  
71.766 Million cell updates/sec

Title: US-09-787-443A-22  
Perfect score: 11  
Sequence: 1 ARKSRDMTAAIK 11

Scoring table: OLIGO  
Gapop 60.0 , Gapext 60.0

Searched: 1586107 seqs, 282547505 residues

Word size : 0

Total number of hits satisfying chosen parameters: 22883

Minimum DB seq length: 11

Maximum DB seq length: 11

Post-processing: Listing first 100 summaries

Database : A\_Geneseq\_29Jan04:\*  
1: geneseqp1980s:\*  
2: geneseqp1990s:\*  
3: geneseqp2000s:\*  
4: geneseqp2001s:\*  
5: geneseqp2002s:\*  
6: geneseqp2003as:\*  
7: geneseqp2003bs:\*  
8: geneseqp2004s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

		8					
Result		Query					
No.	Score	Match	Length	DB	ID	Description	
-----							
1	11	100.0	11	3	AAV88550	Aay88550	NCAM Igl
2	11	100.0	11	5	ABG69350	Abg69350	Human neu
3	4	36.4	11	2	AAR28088	Aar28088	Cell-to-c
4	4	36.4	11	2	AAR37430	Aar37430	Promega p
5	4	36.4	11	2	AAR83762	Aar83762	NGF deriv
6	4	36.4	11	2	AAW09653	Aaw09653	Labelled
7	4	36.4	11	2	AAV31014	Aay31014	Non-cross
8	4	36.4	11	5	AAU78981	Aau78981	Histone H
9	4	36.4	11	5	AAU78982	Aau78982	Histone H

10	4	36.4	11	5	AAO21655	Aao21655	Histone a
11	4	36.4	11	5	ABG71544	Abg71544	Acetyllys
12	4	36.4	11	5	ABG71541	Abg71541	Acetyllys
13	3	27.3	11	1	AAP82047	Aap82047	"Peptide
14	3	27.3	11	1	AAP91264	Aap91264	Tissue pl
15	3	27.3	11	2	AAR06754	Aar06754	Tumour ne
16	3	27.3	11	2	AAR07719	Aar07719	Peptide f
17	3	27.3	11	2	AAR31358	Aar31358	Antimicro
18	3	27.3	11	2	AAR32352	Aar32352	Human Fac
19	3	27.3	11	2	AAR43465	Aar43465	Ro/SSA ep
20	3	27.3	11	2	AAR45170	Aar45170	Listeria
21	3	27.3	11	2	AAR70606	Aar70606	HIV(B35)A
22	3	27.3	11	2	AAR79902	Aar79902	Human FK-
23	3	27.3	11	2	AAR64598	Aar64598	RF-1 pept
24	3	27.3	11	2	AAR96813	Aar96813	Human lam
25	3	27.3	11	2	AAR96812	Aar96812	N.gonorrh
26	3	27.3	11	2	AAR96834	Aar96834	N.gonorrh
27	3	27.3	11	2	AAW15309	Aaw15309	78 kDa gl
28	3	27.3	11	2	AAW32498	Aaw32498	Helicosta
29	3	27.3	11	2	AAW41012	Aaw41012	Anti-glut
30	3	27.3	11	2	AAW40399	Aaw40399	NNOS bind
31	3	27.3	11	2	AAW62282	Aaw62282	Synthetic
32	3	27.3	11	2	AAW41078	Aaw41078	ADPHK pro
33	3	27.3	11	2	AAW46000	Aaw46000	Peptide #
34	3	27.3	11	2	AAW20426	Aay20426	Human mic
35	3	27.3	11	2	AAW61162	Aaw61162	IgE deriv
36	3	27.3	11	2	AAW03092	Aay03092	New nocic
37	3	27.3	11	2	AAW29752	Aay29752	Modified
38	3	27.3	11	2	AAW47615	Aay47615	Immunogen
39	3	27.3	11	2	AAW74077	Aaw74077	Fragment
40	3	27.3	11	2	AAW74135	Aaw74135	GI transp
41	3	27.3	11	2	AAW97473	Aaw97473	Antigenic
42	3	27.3	11	2	AAW97472	Aaw97472	Antigenic
43	3	27.3	11	2	AAW97476	Aaw97476	Antigenic
44	3	27.3	11	2	AAW97477	Aaw97477	Antigenic
45	3	27.3	11	2	AAW97474	Aaw97474	Antigenic
46	3	27.3	11	2	AAW97475	Aaw97475	Antigenic
47	3	27.3	11	2	AAW02916	Aay02916	Fragment
48	3	27.3	11	3	AAW89315	Aay89315	Core poly
49	3	27.3	11	3	AAW81922	Aay81922	Asparagin
50	3	27.3	11	3	AAW81923	Aay81923	Asparagin
51	3	27.3	11	3	AAW81915	Aay81915	Asparagin
52	3	27.3	11	3	AAW81924	Aay81924	Asparagin
53	3	27.3	11	3	AAW81916	Aay81916	Asparagin
54	3	27.3	11	3	AAW81919	Aay81919	Asparagin
55	3	27.3	11	3	AAW81918	Aay81918	Asparagin
56	3	27.3	11	3	AAW81920	Aay81920	Asparagin
57	3	27.3	11	3	AAW81917	Aay81917	Asparagin
58	3	27.3	11	3	AAW81921	Aay81921	Asparagin
59	3	27.3	11	3	AAB16453	Aab16453	Linear pe
60	3	27.3	11	3	AAW88542	Aay88542	NCAM Igl
61	3	27.3	11	3	AAW88549	Aay88549	NCAM Igl
62	3	27.3	11	3	AAB10140	Aab10140	Insertion
63	3	27.3	11	3	AAW93544	Aay93544	Amino aci
64	3	27.3	11	3	AAB09423	Aab09423	Hepatitis
65	3	27.3	11	3	AAW81393	Aay81393	PKC-alpha
66	3	27.3	11	3	AAW54479	Aay54479	Peptide u

67	3	27.3	11	3	AAB29416	Aab29416	Synthetic
68	3	27.3	11	3	AAB26504	Aab26504	Human IgE
69	3	27.3	11	3	AAB08569	Aab08569	Peptide i
70	3	27.3	11	3	AAB08606	Aab08606	Peptide i
71	3	27.3	11	4	AAG65304	Aag65304	Anti-IL-1
72	3	27.3	11	4	AAB55201	Aab55201	Anti-RSV
73	3	27.3	11	4	AAE05275	Aae05275	Human imm
74	3	27.3	11	4	AAG99815	Aag99815	ERA bindi
75	3	27.3	11	4	ABB59308	Abb59308	Drosophil
76	3	27.3	11	4	AAB51034	Aab51034	IgE pepti
77	3	27.3	11	4	AAU16831	Aau16831	Peptide P
78	3	27.3	11	4	AAG62970	Aag62970	Complemen
79	3	27.3	11	4	AAG62982	Aag62982	Complemen
80	3	27.3	11	4	AAG62974	Aag62974	Complemen
81	3	27.3	11	4	AAG62998	Aag62998	Complemen
82	3	27.3	11	4	AAG62984	Aag62984	Complemen
83	3	27.3	11	4	AAG62991	Aag62991	Complemen
84	3	27.3	11	4	AAG62972	Aag62972	Complemen
85	3	27.3	11	4	AAG62976	Aag62976	Complemen
86	3	27.3	11	4	AAG62980	Aag62980	Complemen
87	3	27.3	11	4	AAE05944	Aae05944	Basic ami
88	3	27.3	11	4	AAE05945	Aae05945	Basic ami
89	3	27.3	11	4	AAE12050	Aae12050	Humanised
90	3	27.3	11	4	AAB82287	Aab82287	Phosphory
91	3	27.3	11	4	AAB72872	Aab72872	Human p53
92	3	27.3	11	4	AAB35187	Aab35187	Human Tra
93	3	27.3	11	4	ABB00723	Abb00723	Viral DP1
94	3	27.3	11	4	AAB88242	Aab88242	Hsp-65 pe
95	3	27.3	11	4	AAB88274	Aab88274	Hsp-65 pe
96	3	27.3	11	4	ABP22484	Abp22484	HIV A11 m
97	3	27.3	11	4	ABP23325	Abp23325	HIV A11 m
98	3	27.3	11	4	ABP12972	Abp12972	HIV A02 s
99	3	27.3	11	4	ABP20894	Abp20894	HIV A03 m
100	3	27.3	11	4	ABP22986	Abp22986	HIV A11 m

#### ALIGNMENTS

##### RESULT 1

AAAY88550

ID AAY88550 standard; peptide; 11 AA.

XX

AC AAY88550;

XX

DT 07-AUG-2000 (first entry)

XX

DE NCAM Igl binding peptide #22.

XX

KW NCAM; neural cell adhesion molecule; Igl; immunoglobulin domain 1;

KW neurite outgrowth promoter; proliferation; nerve damage; sclerosis;

KW impaired myelination; stroke; Parkinson's disease; memory; schizophrenia;

KW Alzheimer's disease; diabetes mellitus; circadian clock; nephrosis;

KW treatment; prosthetic nerve guide; treatment; nervous system.

XX

OS Synthetic.

XX

PN WO200018801-A2.  
XX  
PD 06-APR-2000.  
XX  
PF 23-SEP-1999; 99WO-DK000500.  
XX  
PR 29-SEP-1998; 98DK-00001232.  
PR 29-APR-1999; 99DK-00000592.  
XX  
PA (RONN/) RONN L C B.  
PA (BOCK/) BOCK E.  
PA (HOLM/) HOLM A.  
PA (OLSE/) OLSEN M.  
PA (OSTE/) OSTERGAARD S.  
PA (JENS/) JENSEN P H.  
PA (POUL/) POULSEN F M.  
PA (SORO/) SOROKA V.  
PA (RALE/) RALETS I.  
PA (BERE/) BEREZIN V.  
XX  
PI Ronn LCB, Bock E, Holm A, Olsen M, Ostergaard S, Jensen PH;  
PI Poulsen FM, Soroka V, Ralets I, Berezin V;  
XX  
DR WPI; 2000-293111/25.  
XX  
PT Compositions that bind neural cell adhesion molecules useful for treating  
PT disorders of the nervous system and muscles e.g. Alzheimer's and  
PT Parkinson's diseases.  
XX  
PS Example 4; Page 25; 119pp; English.  
XX  
CC Neural cell adhesion molecule (NCAM) is a cellular adhesion molecule.  
CC NCAM is found in three forms, two of which are transmembrane forms, while  
CC the third is attached via a lipid anchor to the cell membrane. All three  
CC NCAM forms have an extracellular structure consisting five immunoglobulin  
CC domains (Ig domains). The Ig domains are numbered 1 to 5 from the N-  
CC terminal. The present sequence represents a peptide which binds to the  
CC NCAM Igl domain. The peptide can be used in a compound which binds to  
CC NCAM-Igl/Ig2 domains, and is capable of stimulating or promoting neurite  
CC outgrowth from NCAM presenting cells, and is also capable of promoting  
CC the proliferation of NCAM presenting cells. The compound may be used in  
CC the treatment of normal, degenerated or damaged NCAM presenting cells.  
CC The compound may in particular be used to treat diseases of the central  
CC and peripheral nervous systems such as post operative nerve damage,  
CC traumatic nerve damage, impaired myelination of nerve fibres, conditions  
CC resulting from a stroke, Parkinson's disease, Alzheimer's disease,  
CC dementias, sclerosis, nerve degeneration associated with diabetes  
CC mellitus, disorders affecting the circadian clock or neuro-muscular  
CC transmission and schizophrenia. Conditions affecting the muscles may also  
CC be treated with the compound, such as conditions associated with impaired  
CC function of neuromuscular connections (e.g. genetic or traumatic shock or  
CC traumatic atrophic muscle disorders). Conditions of the gonads, pancreas  
CC (e.g. diabetes mellitus types I and II), kidney (e.g. nephrosis), heart,  
CC liver and bowel may also be treated using the compound. The compound is  
CC used in a prosthetic nerve guide, and also to stimulate the ability to  
CC learn, and to stimulate the memory of a subject  
XX



SQ Sequence 11 AA;

Query Match 100.0%; Score 11; DB 3; Length 11;  
Best Local Similarity 100.0%; Pred. No. 1.1e-05;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ARKSRDMTAAK 11  
|||||||  
Db 1 ARKSRDMTAAK 11

RESULT 2

ABG69350

ID ABG69350 standard; peptide; 11 AA.

XX

AC ABG69350;

XX

DT 21-OCT-2002 (first entry)

XX

DE Human neural cell adhesion molecule (NCAM) peptide #22.

XX

KW Human; neural cell adhesion molecule; NCAM; heart muscle cell survival;

KW acute myocardial infarction; central nervous system disorder; stroke;

KW peripheral nervous system disorder; postoperative nerve damage;

KW traumatic nerve damage; spinal cord injury; nerve fibre; schizophrenia;

KW postischaemic damage; multiinfarct dementia; multiple sclerosis;

KW nerve degeneration; diabetes mellitus; neuro-muscular degeneration;

KW Alzheimer's disease; Parkinson's disease;

KW Huntington's disease. atrophic muscle disorder; gonad degeneration;

KW nephrosis.

XX

OS Homo sapiens.

XX

PN WO200247719-A2.

XX

PD 20-JUN-2002.

XX

PF 12-DEC-2001; 2001WO-DK000822.

XX

PR 12-DEC-2000; 2000DK-00001863.

XX

PA (ENKA-) ENKAM PHARM AS.

XX

PI Bock E, Berezin V, Kohler LB;

XX

DR WPI; 2002-583473/62.

XX

PT Use of a compound comprising a peptide of neural cell adhesion molecule,

PT in the preparation of medicament for preventing death of cells presenting

PT NCAM or NCAM ligand and treating central nervous system diseases.

XX

PS Disclosure; Page 16; 57pp; English.

XX

CC The invention relates to use of a compound (I) comprising a peptide which

CC comprises at least 5 contiguous amino acid residues of a sequence of the

CC neural cell adhesion molecule (NCAM), its fragment, variant or its mimic,

CC for the preparation of a medicament for preventing death of cells

CC presenting the NCAM or an NCAM ligand. (I) is useful in the preparation  
 CC of a medicament for preventing death of cells presenting the NCAM or an  
 CC NCAM ligand. The medicament is for the stimulation of the survival of  
 CC heart muscle cells, such as survival after acute myocardial infarction.  
 CC The medicament is for the treatment of diseases or conditions of the  
 CC central and peripheral nervous system, such as postoperative nerve  
 CC damage, traumatic nerve damage, e.g. resulting from spinal cord injury,  
 CC impaired myelination of nerve fibres, postischaemic damage, e.g.  
 CC resulting from a stroke, multiinfarct dementia, multiple sclerosis, nerve  
 CC degeneration associated with diabetes mellitus, neuro-muscular  
 CC degeneration, schizophrenia, Alzheimer's disease, Parkinson's disease and  
 CC Huntington's disease. The medicament is for the treatment of diseases or  
 CC conditions of the muscles including conditions with impaired function of  
 CC neuro-muscular connections, such as genetic or traumatic atrophic muscle  
 CC disorders, and for the treatment of diseases of conditions of various  
 CC organs, such as degenerative conditions of the gonads, pancreas (e.g.  
 CC diabetes mellitus type I and II) and kidney (e.g. nephrosis). ABG69329-  
 CC ABG69352 represent human NCAM peptides of the invention  
 XX  
 SQ Sequence 11 AA;

Query Match 100.0%; Score 11; DB 5; Length 11;  
 Best Local Similarity 100.0%; Pred. No. 1.1e-05;  
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ARKSRDMTAAK 11  
 |||||  
 Db 1 ARKSRDMTAAK 11

RESULT 3  
 AAR28088

ID AAR28088 standard; protein; 11 AA.

XX

AC AAR28088;

XX

DT 25-MAR-2003 (revised)

DT 27-NOV-1992 (first entry)

XX

DE Cell-to-cell binding inhibiting peptide subunit (13).

XX

KW Adhesion; integrin; multimer.

XX

OS Synthetic.

XX

FH Key Location/Qualifiers

FT Cross-links 6. .11

FT /note= "sequence linked by interchain amide bond at Lys

FT position to Glu residue on Arg5-Glu-Ser-Arg-Gly-Asp-Val

FT sequence (see AAR28087)"

XX

PN WO9208476-A1.

XX

PD 29-MAY-1992.

XX

PF 07-NOV-1991; 91WO-US008328.

XX

PR 07-NOV-1990; 90US-00610363.  
 XX  
 PA (SCRI ) SCRIPPS RES INST.  
 XX  
 PI Ruggeri ZM, Houghten RA;  
 XX  
 DR WPI; 1992-199940/24.  
 XX  
 PT Peptides inhibiting binding of adhesion mols. to cells expressing  
 PT integrins - for treating and preventing thrombus formation and diseases  
 PT associated with platelet aggregation.  
 XX  
 PS Disclosure; Page 37-38; 70pp; English.  
 XX  
 CC A peptide which inhibits binding of adhesion mols. to cells expressing  
 CC integrins comprises two subunits having the sequences given in AAR28087-  
 CC 88, held together by an interchain stable bond. The sequence RGD is in  
 CC each of the subunits. (Updated on 25-MAR-2003 to correct PN field.)  
 XX  
 SQ Sequence 11 AA;  
  
 Query Match 36.4%; Score 4; DB 2; Length 11;  
 Best Local Similarity 100.0%; Pred. No. 6.2e+02;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
 Qy 2 RKSR 5  
 ||||  
 Db 5 RKSR 8

#### RESULT 4

AAR37430

ID AAR37430 standard; peptide; 11 AA.

XX

AC AAR37430;

XX

DT 25-MAR-2003 (revised)

DT 08-SEP-1993 (first entry)

XX

DE Promega peptide 5.

XX

KW Modified peptide substrate; non-radioactive; detection; dansyl;  
 KW sulphorhodamine 101; lissamine; rhodamine; enzymes; phosphatases;  
 KW protein kinases; proteases.

XX

OS Synthetic.

XX

FH Key Location/Qualifiers.

FT Modified-site 1

FT /note= "detection tag= lissamine, Rhodamine"

XX

PN W09310461-A1.

XX

PD 27-MAY-1993.

XX

PF 12-NOV-1992; 92WO-US009595.

XX

PR 12-NOV-1991; 91US-00791928.  
 XX  
 PA (PROM-) PROMEGA CORP.  
 XX  
 PI Shultz JW, White DH;  
 XX  
 DR WPI; 1993-182698/22.  
 XX  
 PT Quantitating presence or activity of enzyme - by incubating with modified  
 PT peptide substrate and measuring the modified peptide prod.  
 XX  
 PS Claim 24; Page 27; 103pp; English.  
 XX  
 CC Promega peptide 5 is tagged with dansyl at residue 1 and may be used in a  
 CC novel non-radioactive method of quantitating the presence or activity of  
 CC an enzyme. The method can be used for rapid, specific and highly  
 CC sensitive detection of enzymes such as protein kinases, phosphatases and  
 CC proteases, esp. in this case protein kinase C. They can be used to study  
 CC enzyme function in metabolism and in diagnosis of disease. They also  
 CC allow quantitative determ. of the enzyme's activity. See also AAR37426-  
 CC 36. (Updated on 25-MAR-2003 to correct PN field.)  
 XX  
 SQ Sequence 11 AA;

Query Match 36.4%; Score 4; DB 2; Length 11;  
 Best Local Similarity 100.0%; Pred. No. 6.2e+02;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 RKSR 5  
 ||||  
 Db 5 RKSR 8

# RESULT 5

AAR83762

ID AAR83762 standard; peptide; 11 AA.

XX

AC AAR83762;

XX

DT 18-MAR-1996 (first entry)

XX

DE NGF derived structural analog C(29-35deltaD30A).

XX

KW Neurotrophin receptor; structural analog; nerve growth factor; beta turn;

KW reverse turn; cyclic; tracer; uncharged; hydrophobic; inhibition;

KW neurite outgrowth; central nervous system; peripheral nervous system;

KW tumour; neuroma; hormone-receptor interaction site; immunisation;

KW receptor domain-function correlation.

XX

OS Synthetic.

XX

FH Key Location/Qualifiers

FT Modified-site 1

FT /note= "contains Fmoc protective group "

FT Misc-difference 1

FT /note= "any uncharged or hydrophobic amino acid"

FT Misc-difference 11

FT /note= "any uncharged or hydropathic amino acid"  
 XX  
 PN WO9521193-A1.  
 XX  
 PD 10-AUG-1995.  
 XX  
 PF 07-FEB-1995; 95WO-CA000059.  
 XX  
 PR 07-FEB-1994; 94GB-00002331.  
 XX  
 PA (UYMC-) UNIV MCGILL.  
 XX  
 PI Saragovi UH, Lesauteur L, Cuello AC;  
 XX  
 DR WPI; 1995-283731/37.  
 XX  
 PT New cyclic peptide(s) which bind to neurotrophin receptor and mimic or  
 PT inhibit neurotrophin activity - useful e.g. for inhibiting neurite  
 PT outgrowth or treating nervous system disease, tumours, etc.  
 XX  
 PS Claim 9; Page 32; 42pp; English.  
 XX  
 CC The peptides AAR83760-80 are examples of peptides that bind to the  
 CC neurotrophin receptor under physiological conditions in vivo or in vitro.  
 CC The peptides are structural analogs of nerve growth factor (NGF) and  
 CC contain at least one beta turn (from region 28-36, 43-49 or 91-98) or 3  
 CC consecutive reverse turns (from region 59-65). The peptides may be  
 CC cyclised by oxidn. of Cys or other cyclisation procedure and may be  
 CC linked to a tracer e.g. a metal chelate or radionuclide. The peptides may  
 CC contain uncharged or hydropathic amino acids at the N- and C-termini,  
 CC which are optionally protected by an Fmoc or acetyl protecting group. The  
 CC peptides are useful for inhibition of neurotrophin, esp. for inhibiting  
 CC neurite outgrowth, treating central or peripheral nervous system disease,  
 CC tumours and neuromas, for mapping hormone-receptor interaction sites and  
 CC receptor domain-function correlation and for immunisation. This peptide  
 CC is derived from residues 29-35 with a substitution of residue 30 Asp for  
 CC Ala, and contains a beta turn  
 XX  
 SQ Sequence 11 AA;

Query Match 36.4%; Score 4; DB 2; Length 11;  
 Best Local Similarity 100.0%; Pred. No. 6.2e+02;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 TAIK 11  
 ||||  
 Db 3 TAIK 6

RESULT 6  
 AAW09653  
 ID AAW09653 standard; peptide; 11 AA.  
 XX  
 AC AAW09653;  
 XX  
 DT 25-MAR-2003 (revised)  
 DT 20-MAY-1997 (first entry)

XX  
DE Labelled peptide substrate used in enzyme activity assay.  
XX  
KW Enzyme activity; assay; measurement; label; rhodamine; dansyl;  
KW non-radioactive; electrophoretic separation; protein kinase; protease;  
KW phosphatase.  
XX  
OS Synthetic.  
XX  
FH Key Location/Qualifiers  
FT Modified-site 1  
FT /note= "labelled with rhodamine B detection tag"  
XX  
PN US5580747-A.  
XX  
PD 03-DEC-1996.  
XX  
PF 21-JAN-1994; 94US-00185448.  
XX  
PR 12-NOV-1991; 91US-00791928.  
XX  
PA (PROM-) PROMEGA CORP.  
XX  
PI White DH, Shultz JW;  
XX  
DR WPI; 1997-033568/03.  
XX  
PT Non:radioactive assay for measuring enzyme activity - involving  
PT electrophoretic sepn. of labelled cleavage prod. from labelled peptide  
PT substrate.  
XX  
PS Claim 5; Col 39-40; 35pp; English.  
XX  
CC AAW09653 is a peptide substrate used in a non-radioactive assay for  
CC measuring enzyme activity. The assay comprises incubating the enzyme with  
CC the labelled peptide substrate to form a labelled peptide product;  
CC separating the product from the substrate by agarose gel electrophoresis  
CC and measuring the amount of product by detecting the label by  
CC fluorescence or chemiluminescence. The assay can be performed rapidly and  
CC with great sensitivity. This peptide is especially for determining  
CC protein kinase C activity, e.g. to study its function in metabolism or to  
CC screen for potential inhibitors. (Updated on 25-MAR-2003 to correct PF  
CC field.)  
XX  
SQ Sequence 11 AA;

Query Match 36.4%; Score 4; DB 2; Length 11;  
Best Local Similarity 100.0%; Pred. No. 6.2e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 RKSR 5  
||||  
Db 5 RKSR 8

RESULT 7  
AAY31014

ID AAY31014 standard; peptide; 11 AA.  
 XX  
 AC AAY31014;  
 XX  
 DT 21-OCT-1999 (first entry)  
 XX  
 DE Non-crosslinked protein particle peptide 63.  
 XX  
 KW Non-crosslinked protein particle; diagnostic; therapy; monodisperse;  
 KW albumin; haemoglobin; nanometer; micrometer; clearance.  
 XX  
 OS Synthetic.  
 XX  
 PN US5945033-A.  
 XX  
 PD 31-AUG-1999.  
 XX  
 PF 12-NOV-1996; 96US-00747137.  
 XX  
 PR 15-JAN-1991; 91US-00641720.  
 PR 13-OCT-1992; 92US-00959560.  
 PR 01-JUN-1993; 93US-00069831.  
 PR 14-MAR-1994; 94US-00212546.  
 XX  
 PA (HEMO-) HEMOSPHERE INC.  
 XX  
 PI Yen RCK;  
 XX  
 DR WPI; 1999-508153/42.  
 XX  
 PT Non-crosslinked protein particles for therapeutic and diagnostic use.  
 XX  
 PS Example 22; Col 77-78; 65pp; English.  
 XX  
 CC This invention describes a novel aqueous suspension of monodisperse  
 CC particles on non-crosslinked, non-denatured albumin (50-5000 nm) which is  
 CC stable against dissolving upon dilution with an alcohol-free aqueous  
 CC medium. The method involves (a) forming an aqueous solution containing  
 CC albumin and hemoglobin and (b) treating the aqueous solution with an  
 CC alcohol to cause the solution to become turbid. The particles are useful  
 CC as agents for in vivo administration, either of their own administration  
 CC or as a vehicle for other therapeutic or diagnostic agents. The method  
 CC permits the formation of albumin and hemoglobin particles in the  
 CC nanometer and micrometer size range, in a form closer to their natural  
 CC form than the forms of the prior art. The particles therefore constitute  
 CC a more closely controlled agent for in vivo administration, with greater  
 CC ease of clearance from the body after their period of usefulness.  
 CC AAY30952-Y31135 represent peptides used in the method of the invention  
 XX  
 SQ Sequence 11 AA;

Query Match 36.4%; Score 4; DB 2; Length 11;  
 Best Local Similarity 100.0%; Pred. No. 6.2e+02;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 RKSR 5  
 ||||

## RESULT 8

AAU78981

ID AAU78981 standard; peptide; 11 AA.

XX

AC AAU78981;

XX

DT 18-JUN-2002 (first entry)

XX

DE Histone H3 antigenic fragment #5.

XX

KW Histone; antibody; antigen; methyllysine; gene activation;

KW gene repression; heterochromatin; euchromatin; histone methylation;

KW genetic imprinting; gene silencing.

XX

OS Synthetic.

XX

FH Key Location/Qualifiers

FT Modified-site 5

FT /note= "Lys is methylated"

XX

PN WO200218418-A1.

XX

PD 07-MAR-2002.

XX

PF 23-AUG-2001; 2001WO-US026283.

XX

PR 25-AUG-2000; 2000US-0227767P.

PR 03-JUL-2001; 2001US-0302747P.

XX

PA (UYVI-) UNIV VIRGINIA PATENT FOUND.

XX

PI Allis CD, Strahl BD;

XX

DR WPI; 2002-315534/35.

XX

PT New methyllysine-specific antibodies, useful for as diagnostic or  
PT screening tools, as well as in identifying regions of heterochromatin or  
PT euchromatin.

XX

PS Claim 1; Page 9; 60pp; English.

XX

CC This invention relates to novel methyllysine histone antibodies which  
CC specifically bind to histones H3 and H4. The present invention is  
CC directed to post translational modifications of histones, in particular  
CC the methylation of lysine residues. Methylation of histones has been  
CC shown to be important for gene activation and repression. The antibodies  
CC are useful in identifying regions of heterochromatin or euchromatin. The  
CC antibodies are also useful as diagnostic or screening tools. The  
CC antibodies may also be used to analyse chromosomes for regions of  
CC transcriptional activity according to differential methylation and also  
CC in studies of genetic imprinting and gene silencing. The antibodies may  
CC also be useful for studying diseases linked to imprinting such as Prader-  
CC Willi syndrome or Angelman syndrome. The present sequence represents the  
CC histone antigenic fragment #5 specific for the N terminal of histone H3



CC used to generate anti histone antibodies of the invention

XX

SQ Sequence 11 AA;

Query Match 36.4%; Score 4; DB 5; Length 11;

Best Local Similarity 100.0%; Pred. No. 6.2e+02;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ARKS 4

||||

Db 3 ARKS 6

# RESULT 9

AAU78982

ID AAU78982 standard; peptide; 11 AA.

XX

AC AAU78982;

XX

DT 18-JUN-2002 (first entry)

XX

DE Histone H3 antigenic fragment #6.

XX

KW Histone; antibody; antigen; methyllysine; gene activation;

KW gene repression; heterochromatin; euchromatin; histone methylation;

KW genetic imprinting; gene silencing.

XX

OS Synthetic.

XX

FH Key Location/Qualifiers

FT Modified-site 5

FT /note= "Lys is methylated"

XX

PN WO200218418-A1.

XX

PD 07-MAR-2002.

XX

PF 23-AUG-2001; 2001WO-US026283.

XX

PR 25-AUG-2000; 2000US-0227767P.

PR 03-JUL-2001; 2001US-0302747P.

XX

PA (UYVI-) UNIV VIRGINIA PATENT FOUND.

XX

PI Allis CD, Strahl BD;

XX

DR WPI; 2002-315534/35.

XX

PT New methyllysine-specific antibodies, useful for as diagnostic or

PT screening tools, as well as in identifying regions of heterochromatin or

PT euchromatin.

XX

PS Claim 1; Page 9; 60pp; English.

XX

CC This invention relates to novel methyllysine histone antibodies which

CC specifically bind to histones H3 and H4. The present invention is

CC directed to post translational modifications of histones, in particular

CC the methylation of lysine residues. Methylation of histones has been  
 CC shown to be important for gene activation and repression. The antibodies  
 CC are useful in identifying regions of heterochromatin or euchromatin. The  
 CC antibodies are also useful as diagnostic or screening tools. The  
 CC antibodies may also be used to analyse chromosomes for regions of  
 CC transcriptional activity according to differential methylation and also  
 CC in studies of genetic imprinting and gene silencing. The antibodies may  
 CC also be useful for studying diseases linked to imprinting such as Prader-  
 CC Willi syndrome or Angelman syndrome. The present sequence represents the  
 CC histone antigenic fragment #6 specific for the N terminal of histone H3  
 CC used to generate anti histone antibodies of the invention  
 XX  
 SQ Sequence 11 AA;

Query Match 36.4%; Score 4; DB 5; Length 11;  
 Best Local Similarity 100.0%; Pred. No. 6.2e+02;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ARKS 4  
 ||||  
 Db 3 ARKS 6

RESULT 10  
 AAO21655

ID AAO21655 standard; peptide; 11 AA.  
 XX  
 AC AAO21655;  
 XX  
 DT 05-SEP-2002 (first entry)  
 XX  
 DE Histone acetyltransferase inhibitor related peptide-alternative SEQ ID 7.  
 XX  
 KW Cytostatic; amide derivative; coenzyme A; CoA; acetyltransferase; cancer;  
 KW gene therapy; enzyme inhibitor.  
 XX  
 OS Unidentified.  
 XX  
 FH Key Location/Qualifiers  
 FT Modified-site 1  
 FT /note= "This residue is acetylated"  
 XX  
 PN US6369030-B1.  
 XX  
 PD 09-APR-2002.  
 XX  
 PF 29-NOV-1999; 99US-00451034.  
 XX  
 PR 29-NOV-1999; 99US-00451034.  
 XX  
 PA (UYRQ ) UNIV ROCKEFELLER.  
 XX  
 PI Cole PA, Soccio RE, Lau OD, Khalil EM, Kundu TK, Roeder RG;  
 XX  
 DR WPI; 2002-506396/54.  
 XX  
 PT New amide derivatives comprising coenzyme A are histone acetyltransferase

PT inhibitors useful in e.g. the treatment of cancers and gene therapy.  
XX  
PS Claim 2; Col 20; 20pp; English.  
XX  
CC The invention relates to novel amide derivatives comprising coenzyme A  
CC (CoA). The amide derivatives of the invention can be used for inhibiting  
CC acetyltransferase in diseased cells and treating e.g. cancer, and also  
CC for use in gene therapy. This sequence represents an alternative version  
CC of peptide SEQ ID No7, which is part of a synthetic molecule that acts as  
CC an enzyme inhibitor relating to the invention  
XX  
SQ Sequence 11 AA;

Query Match 36.4%; Score 4; DB 5; Length 11;  
Best Local Similarity 100.0%; Pred. No. 6.2e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ARKS 4  
| | | |  
Db 6 ARKS 9

RESULT 11

ABG71544

ID ABG71544 standard; peptide; 11 AA.

XX

AC ABG71544;

XX

DT 31-DEC-2002 (first entry)

XX

DE Acetyllysine-containing peptide H3-23-TKA used in ELISA assay.

XX

KW Mouse; anti-acetyllysine monoclonal antibody; N epsilon-acetyllysine;

KW functional analysis; acetyllysine-containing protein; pathosis;

KW acetylated protein; disease diagnosis; histone acetylation; mAb;

KW antibody-producing immortalised cell.

XX

OS Unidentified.

XX

FH Key Location/Qualifiers

FT Modified-site 4

FT /note= "Modified by acetyl (Ac) group"

XX

PN WO200274962-A1.

XX

PD 26-SEP-2002.

XX

PF 13-MAR-2002; 2002WO-JP002330.

XX

PR 15-MAR-2001; 2001JP-00074263.

XX

PA (NISC-) JAPAN SCI & TECHNOLOGY CORP.

PA (NIHA ) JAPAN ENERGY CORP.

XX

PI Komatsu Y, Yoshida M;

XX

DR WPI; 2002-750555/81.

XX  
PT Production of anti-acetyllysine monoclonal antibody capable of  
PT recognizing N epsilon-acetyllysine regardless of types of adjacent  
PT amino acids, useful in e.g. disease diagnosis and searching for novel  
PT acetyllysine-containing proteins.  
XX  
PS Example 1; Page 7; 45pp; Japanese.  
XX  
CC The present invention relates to a mouse anti-acetyllysine monoclonal  
CC antibody (mAb) capable of recognising N epsilon-acetyllysine, and a  
CC method for producing the monoclonal antibody. The produced antibody is  
CC useful in searching for and functional analysis of novel acetyllysine-  
CC containing proteins particularly in studying pathosis due to acetylated  
CC proteins, disease diagnosis, facilitating detection of variation in  
CC acetylation levels of histone influenced by various stimulations during  
CC Western blotting, analysis of the variable region in the DNA sequence of  
CC an antibody gene of an antibody-producing immortalised cell, and judging  
CC the degree of homology specific to the sequence during the protein  
CC translation. The monoclonal antibody of the invention is capable of  
CC recognising N epsilon-acetyllysine regardless of the type of adjacent  
CC amino acids and accepting adjacent amino acids over a broad range.  
CC ABG71537-ABG71550 represent acetyllysine-containing peptides used for the  
CC comparison of reactivities in enzyme linked immunosorbent assay (ELISA)  
CC tests with mouse anti-acetyllysine monoclonal antibodies of the invention  
XX  
SQ Sequence 11 AA;

Query Match 36.4%; Score 4; DB 5; Length 11;  
Best Local Similarity 100.0%; Pred. No. 6.2e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ARKS 4  
| | | |  
Db 6 ARKS 9

RESULT 12  
ABG71541  
ID ABG71541 standard; peptide; 11 AA.  
XX  
AC ABG71541;  
XX  
DT 31-DEC-2002 (first entry)  
XX  
DE Acetyllysine-containing peptide H3-9-RKS used in ELISA assay.  
XX  
KW Mouse; anti-acetyllysine monoclonal antibody; N epsilon-acetyllysine;  
KW functional analysis; acetyllysine-containing protein; pathosis;  
KW acetylated protein; disease diagnosis; histone acetylation; mAb;  
KW antibody-producing immortalised cell.  
XX  
OS Unidentified.  
XX  
FH Key Location/Qualifiers  
FT Modified-site 4  
FT /note= "Modified by acetyl (Ac) group"  
XX

PN WO200274962-A1.  
 XX  
 PD 26-SEP-2002.  
 XX  
 PF 13-MAR-2002; 2002WO-JP002330.  
 XX  
 PR 15-MAR-2001; 2001JP-00074263.  
 XX  
 PA (NISC-) JAPAN SCI & TECHNOLOGY CORP.  
 PA (NIHA ) JAPAN ENERGY CORP.  
 XX  
 PI Komatsu Y, Yoshida M;  
 XX  
 DR WPI; 2002-750555/81.  
 XX  
 PT Production of anti-acetyllysine monoclonal antibody capable of  
 PT recognizing N approximately i-acetyllysine regardless of types of adjacent  
 PT amino acids, useful in e.g. disease diagnosis and searching for novel  
 PT acetyllysine-containing proteins.  
 XX  
 PS Example 1; Page 7; 45pp; Japanese.  
 XX  
 CC The present invention relates to a mouse anti-acetyllysine monoclonal  
 CC antibody (mAb) capable of recognising N epsilon-acetyllysine, and a  
 CC method for producing the monoclonal antibody. The produced antibody is  
 CC useful in searching for and functional analysis of novel acetyllysine-  
 CC containing proteins particularly in studying pathosis due to acetylated  
 CC proteins, disease diagnosis, facilitating detection of variation in  
 CC acetylation levels of histone influenced by various stimulations during  
 CC Western blotting, analysis of the variable region in the DNA sequence of  
 CC an antibody gene of an antibody-producing immortalised cell, and judging  
 CC the degree of homology specific to the sequence during the protein  
 CC translation. The monoclonal antibody of the invention is capable of  
 CC recognising N epsilon-acetyllysine regardless of the type of adjacent  
 CC amino acids and accepting adjacent amino acids over a broad range.  
 CC ABG71537-ABG71550 represent acetyllysine-containing peptides used for the  
 CC comparison of reactivities in enzyme linked immunosorbent assay (ELISA)  
 CC tests with mouse anti-acetyllysine monoclonal antibodies of the invention  
 XX  
 SQ Sequence 11 AA;

Query Match 36.4%; Score 4; DB 5; Length 11;  
 Best Local Similarity 100.0%; Pred. No. 6.2e+02;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ARKS 4  
 ||||  
 Db 2 ARKS 5

RESULT 13  
 AAP82047  
 ID AAP82047 standard; peptide; 11 AA.  
 XX  
 AC AAP82047;  
 XX  
 DT 19-OCT-1990 (first entry)

XX  
 DE "Peptide 2" consisting of residues Arg15 to Arg25 of amyloid A protein.  
 XX  
 KW Amyloid A protein; secondary amyloidosis; anti-amyloid A antibody.  
 XX  
 OS Synthetic.  
 XX  
 PN JP63044895-A.  
 XX  
 PD 25-FEB-1988.  
 XX  
 PF 13-AUG-1986; 86JP-00189810.  
 XX  
 PR 13-AUG-1986; 86JP-00189810.  
 XX  
 PA (KYOW ) KYOWA HAKKO KOGYO KK.  
 XX  
 DR WPI; 1988-094820/14.  
 XX  
 PT Anti-amyloid-A protein monoclonal antibody - used esp. for detection of  
 PT sec. amyloidosis.  
 XX  
 PS Claim 2; Page 649; 6pp; Japanese.  
 XX  
 CC An antibody capable of recognising Amyloid A and peptide 3 (His37 to  
 CC Arg47) derived from Amyloid A, but which does not react with other  
 CC specified peptides (including peptide 2) is useful for detection of  
 CC secondary amyloidosis. See also AAP82045-6 and AAP82048-9  
 XX  
 SQ Sequence 11 AA;  
  
 Query Match 27.3%; Score 3; DB 1; Length 11;  
 Best Local Similarity 100.0%; Pred. No. 7.9e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
 Qy 5 RDM 7  
 |||  
 Db 1 RDM 3

# RESULT 14

AAP91264

ID AAP91264 standard; peptide; 11 AA.  
 XX  
 AC AAP91264;  
 XX  
 DT 25-MAR-2003 (revised)  
 DT 20-DEC-1989 (first entry)  
 XX  
 DE Tissue plasminogen activator mutant EGAV (V51R: N451Q).  
 XX  
 KW Tissue plasminogen activator; mutant; fibrinolysis; EGAV (V51R: N451Q).  
 XX  
 OS Homo sapiens.  
 XX  
 FH Key Location/Qualifiers  
 FT Modified-site 7

XX  
 PN WO8907146-A.  
 XX  
 PD 10-AUG-1989.  
 XX  
 PF 03-FEB-1989; 89WO-US000465.  
 XX  
 PR 05-FEB-1988; 88US-00152692.  
 XX  
 PA (INTE-) INTEG GENETICS INC.  
 XX  
 PI Markland W, Livingston DJ;  
 XX  
 DR WPI; 1989-249015/34.  
 XX  
 PT Rearranged tissue plasminogen activators - prepd. by altering the DNA  
 PT sequence to introduce Avr II, Nhe I, Spe I or Xba I cleavage sites.  
 XX  
 PS Disclosure; Page 36; 77pp; English.  
 XX  
 CC The peptide is encoded by AAN90545. The peptide has tPA activity, with  
 CC extended in vivo half life. Spacing between tPA domains is increased, to  
 CC increase rate of fibrinolysis or the resistance to inhibition by  
 CC endogenous tPA inhibitors present in human plasma. The peptide is used  
 CC for thrombolysis in the treatment of myocardial infarction, pulmonary  
 CC embolism, deep vein thrombosis and stroke. See also AAP91265-84. (Updated  
 CC on 25-MAR-2003 to correct PA field.)  
 XX  
 SQ Sequence 11 AA;

Query Match 27.3%; Score 3; DB 1; Length 11;  
 Best Local Similarity 100.0%; Pred. No. 7.9e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 RKS 4  
 |||  
 Db 7 RKS 9

# RESULT 15

AAR06754

ID AAR06754 standard; protein; 11 AA.

XX

AC AAR06754;

XX

DT 25-MAR-2003 (revised)

DT 23-OCT-1990 (first entry)

XX

DE Tumour necrosis factor derived peptide.

XX

KW Tumour necrosis factor; TNF; neoplastic disease; autoimmune disease;  
 KW infection; inflammation; transplant rejection.

XX

OS Synthetic.

XX

FH Key Location/Qualifiers

FT Misc-difference 5. .5

FT /label= K, Q, R  
 XX  
 PN DE3841753-A.  
 XX  
 PD 13-JUN-1990.  
 XX  
 PF 12-DEC-1988; 88DE-03841753.  
 XX  
 PR 12-DEC-1988; 88DE-03841753.  
 XX  
 PA (BADI ) BASF AG.  
 PA (BOEH/) BOEHR H J.  
 XX  
 PI Bohm HJ, Daum L, Schmied B, Walker N, Zechel JC, Haupt A;  
 XX  
 DR WPI; 1990-186573/25.  
 XX  
 PT New tumour necrosis factor derived peptide(s) - for treating or  
 PT preventing neoplastic and auto-immune disease, infection, inflammation  
 PT and transplant rejection.  
 XX  
 PS Example 67; Page 11; 15pp; German.  
 XX  
 CC To residue F1 is attached Ac and to residue A11 NH2. A3 and K9 form  
 CC together a covalent bond. This peptide is an example of a highly generic  
 CC sequence of the formula X-A-G-D-Y. A= K,Q or R; X= G-NH-CHM-CO, G-NH-CHM-  
 CC CO-W, G-R-NH-CHM-CO or G-R-NH-CHM-CO-W; Y= Z, NH-CHQ-COZ, V-NH-CHQ-COZ,  
 CC NH-CHQ-CO-U-Z or V-NH-CHQ-CO-U-Z; G= H or an amino protecting group; Z=  
 CC OH, NH2 or carboxy protecting group; or G and Z together are a covalent  
 CC bond or the gp. CO(CH2)aNH; a=1-12; R,U,V and W= peptide chains of 1-4  
 CC naturally occurring alpha aminoacids; M and Q= H, isopropyl, CHMe.Et,  
 CC phenyl, CH(OH).Me, 3-indolyl- or 4-imidazolyl-methyl or (CH2)bT; b=1-6; T=  
 CC OH, MeO, MeS, Me2CH, phenyl (opt. 4-OH, substd), HS, NH2, COOH, CONH2, NH  
 CC C (NH) NH2; or M and Q together are (CH2)c-S-S-(CH2)d, (CH2)eCO NH-(CH2)f  
 CC or (CH2)eNH CO(CH2)gNH CO(CH2) f; c and d=1-4; e and f=1-6; g=1-12. The  
 CC peptide is a low mol. wt. deriv. of TNF. See also DE3841753-55,  
 CC DE3841759, DE3841761-64, DE3841767-68. (Updated on 25-MAR-2003 to correct  
 CC PA field.)  
 XX  
 SQ Sequence 11 AA;

Query Match 27.3%; Score 3; DB 2; Length 11;  
 Best Local Similarity 100.0%; Pred. No. 7.9e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 RKS 4  
 |||  
 Db 8 RKS 10

RESULT 16  
 AAR07719  
 ID AAR07719 standard; protein; 11 AA.  
 XX  
 AC AAR07719;  
 XX  
 DT 25-MAR-2003 (revised)



DT 22-FEB-1991 (first entry)  
 XX  
 DE Peptide fragment #5 from protease inhibitor Gelin.  
 XX  
 KW Gelin; protease inhibitor; Buffalo leeches; peridontal disease;  
 KW pulmonary emphysema; antibiotic.  
 XX  
 OS Hirudinaria manillensis.  
 XX  
 FH Key Location/Qualifiers  
 FT Misc-difference 1  
 FT /label= Asn, Ser  
 XX  
 PN WO9012808-A.  
 XX  
 PD 01-NOV-1990.  
 XX  
 PF 14-APR-1989; 89NL-00000943.  
 XX  
 PR 14-APR-1989; 89NL-00000943.  
 XX  
 PA (EUBI-) EURO-BIOPHARM TECHN.  
 XX  
 PI Atkinson A, Electricwa A, Sawyer RT, Vonsicard N, Voerman G;  
 XX  
 DR WPI; 1990-348426/46.  
 XX  
 PT Protease-inhibitor, gelin - is used in pharmaceutical, cosmetic and  
 PT dental compsns.  
 XX  
 PS Claim 3; Page 39; 57pp; English.  
 XX  
 CC The sequence is one of 6 fragments from Gelin, a protein with strong anti  
 CC -elastase and anti-chymotrypsin activity. Gelin is used to treat  
 CC periodontal diseases in mammals and can be used as an antibiotic against  
 CC bacteria. It may also inhibit germination of grains and seeds. The  
 CC polypeptide is isolated from leeches of the subfamily Hirudinariae  
 CC ("Buffalo leeches"). The identity of residue 6 is unknown. See also  
 CC AAR07714-8 and AAR07720. (Updated on 25-MAR-2003 to correct PA field.)  
 CC (Updated on 25-MAR-2003 to correct PI field.)  
 XX  
 SQ Sequence 11 AA;

Query Match 27.3%; Score 3; DB 2; Length 11;  
 Best Local Similarity 100.0%; Pred. No. 7.9e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 DMT 8  
 |||  
 Db 9 DMT 11

RESULT 17  
 AAR31358  
 ID AAR31358 standard; peptide; 11 AA.  
 XX  
 AC AAR31358;

XX  
 DT 25-MAR-2003 (revised)  
 DT 20-MAY-1998 (first entry)  
 XX  
 DE Antimicrobial peptide #12 derived from bovine lactoferrin.  
 XX  
 KW antimicrobial agent; iron-binding protein; athlete's foot; mastitis;  
 KW antibacterial agent.  
 XX  
 OS Synthetic.  
 XX  
 PN EP503939-A1.  
 XX  
 PD 16-SEP-1992.  
 XX  
 PF 12-MAR-1992; 92EP-00302125.  
 XX  
 PR 13-MAR-1991; 91JP-00048196.  
 PR 24-APR-1991; 91JP-00094492.  
 PR 24-APR-1991; 91JP-00094493.  
 XX  
 PA (MORG ) MORINAGA MILK IND CO LTD.  
 XX  
 PI Tomita M, Kawase K, Takase M, Bellamy WR, Yamauchi K;  
 PI Wakabayashi H, Tokita Y;  
 XX  
 DR WPI; 1992-310006/38.  
 XX  
 PT New antimicrobial peptide(s) - active against e.g. *Listeria*  
 PT *monocytogenes*, *Staphylococcus aureus*, *Pseudomonas aeruginosa* and  
 PT *Klebsiella pneumoniae*, for treating e.g. diarrhoea, mastitis, etc.  
 XX  
 PS Claim 8; Page 17; 19pp; English.  
 XX  
 CC This synthetic peptide has a sequence derived from bovine lactoferrin.  
 CC The peptide has stronger antimicrobial activity than unhydrolysed  
 CC lactoferrin and improved heat resistance. The peptide had a minimum  
 CC inhibitory concentration (microM) of 1.5, 3, 6 and 25 against *Listeria*  
 CC *monocytogenes*, *Staphylococcus aureus*, *Pseudomonas aeruginosa* and  
 CC *Klebsiella pneumoniae*, respectively. This and other peptides derived from  
 CC hydrolysed lactoferrin can be incorporated into foods, human or  
 CC veterinary compositions (e.g. for treating mastitis and athlete's foot),  
 CC toiletries, cosmetics, cleaning agents, etc. See AAR31350-R31361.  
 CC (Updated on 25-MAR-2003 to correct PN field.)  
 XX  
 SQ Sequence 11 AA;

Query Match 27.3%; Score 3; DB 2; Length 11;  
 Best Local Similarity 100.0%; Pred. No. 7.9e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 KSR 5  
 |||  
 Db 1 KSR 3

RESULT 18

AAR32352

ID AAR32352 standard; peptide; 11 AA.

XX

AC AAR32352;

XX

DT 05-JUL-1993 (first entry)

XX

DE Human Factor X peptide.

XX

KW Anticoagulant; intrinsic; extrinsic; prothrombin activation; thrombin;

KW formation; Factor Xa; pathway mediated activation; inhibition.

XX

OS Synthetic.

XX

PN US5187155-A.

XX

PD 16-FEB-1993.

XX

PF 23-JUN-1989; 89US-00371561.

XX

PR 23-JUN-1989; 89US-00371561.

XX

PA (TEXA ) UNIV TEXAS SYSTEM.

XX

PI Fair DS;

XX

DR WPI; 1993-075751/09.

XX

PT Compsns. comprising peptide(s) of 10-50 aminoacid residues - inhibit

PT factor X activation and/or Factor Xa function, useful for preventing

PT blood clot formation and treating deep vein thrombosis, pulmonary

PT embolism, etc.

XX

PS Example; Page 6; 23pp; English.

XX

CC The sequence is that of a peptide corresponding to amino acids 404-414 of

CC the human factor X molecule which was tested for its effect, (as a % of

CC the control rate), on the rate of Factor Xa formation and on the rate of

CC thrombin formation. The results obt'd. were for activation of Factor X by

CC the extrinsic activation complex 78%, by the intrinsic activation complex

CC 98%, and activation by RVV-X, 76%. For the rate of thrombin formation the

CC rate was 88% as compared to the control rate

XX

SQ Sequence 11 AA;

Query Match 27.3%; Score 3; DB 2; Length 11;

Best Local Similarity 100.0%; Pred. No. 7.9e+03;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ARK 3

|||

Db 1 ARK 3

RESULT 19

AAR43465

ID AAR43465 standard; peptide; 11 AA.

XX  
 AC AAR43465;  
 XX  
 DT 25-MAR-2003 (revised)  
 DT 12-MAY-1994 (first entry)  
 XX  
 DE Ro/SSA epitope 280.  
 XX  
 KW Linear; epitope; 60 kD; Ro/SSA; La/SSB; autoantigen; E/F; G; 70 kD;  
 KW nuclear ribonucleoprotein; nRNP; Sm B/B'; polypeptide; antigen; D;  
 KW systemic lupus erythematosus; SLE; autoantibody; U4/U6; U5; B; B';  
 KW RNA polymerase III; U1; U2; Sjogrens syndrome; SS; human; vaccine; ss.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO9321223-A1.  
 XX  
 PD 28-OCT-1993.  
 XX  
 PF 13-APR-1993; 93WO-US003484.  
 XX  
 PR 13-APR-1992; 92US-00867819.  
 XX  
 PA (OKLA ) UNIV OKLAHOMA STATE.  
 XX  
 PI Harley JB;  
 XX  
 DR WPI; 1993-351658/44.  
 XX  
 PT New linear epitope(s) for human auto-antibodies - from the Ro/SSA, La/SSB  
 PT and Sm B/B' antigens and ribo:nucleoprotein, used for diagnosing and  
 PT treating auto-immune disorders e.g. systemic lupus erythematosus.  
 XX  
 PS Claim 1; Page 31; 43pp; English.  
 XX  
 CC The sequences given in AAR43391-562 are linear epitopes which are derived  
 CC from the 60 kD Ro/SSA peptide, the La/SSB autoantigen, the 70 kD nuclear  
 CC ribonucleoprotein (nRNP) and the Sm B/B' polypeptide. These antigens are  
 CC common in systemic lupus erythematosus (SLE) and closely related  
 CC disorders. The Ro/SSA family of proteins has been shown to have several  
 CC molecular forms which are defined by the molecular weight of the antigen  
 CC identified. The major form has a molecular weight of 60 kD and two  
 CC additional forms have molecular weights of 52 and 54 kD. La/SSB is also a  
 CC member of this group of autoantibodies and binds small RNAs with a  
 CC polyuridine terminus. La/SSB is bound by a third of the anti-Ro/SSA  
 CC precipitin positive sera. La/SSB has been shown to be a 46-50 kD  
 CC monomeric phosphoprotein which associates with RNA polymerase III  
 CC transcripts. Anti-Sm antibodies precipitate snRNPs containing the U1, U2,  
 CC U4/U6 and U5 RNA. Anti-Sm antibodies may be directed against one or a  
 CC combination of the polypeptides: B (26 kD), B' (27 kD), D (13 kD), E/F  
 CC (11 kD doublet) and G (less than 10 kD). These epitopes may be used for  
 CC preventing, treating or screening autoimmune disorders, especially SLE or  
 CC Sjogrens syndrome (SS). They bind to a human autoantibody and may  
 CC therefore be used as vaccines. (Updated on 25-MAR-2003 to correct PN  
 CC field.)  
 XX  
 SQ Sequence 11 AA;

Query Match 27.3%; Score 3; DB 2; Length 11;  
Best Local Similarity 100.0%; Pred. No. 7.9e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 MTA 9  
   | | |  
Db 9 MTA 11

RESULT 20

AAR45170

ID AAR45170 standard; protein; 11 AA.

XX

AC AAR45170;

XX

DT 25-MAR-2003 (revised)

DT 16-JUN-1994 (first entry)

XX

DE Listeria p60 peptide epitope.

XX

KW Listeria monocytogenes; antibodies; immunoassay; conjugate.

XX

OS Synthetic.

XX

PN DE4318450-A1.

XX

PD 16-DEC-1993.

XX

PF 03-JUN-1993; 93DE-04318450.

XX

PR 11-JUN-1992; 92DE-04219111.

PR 25-NOV-1992; 92DE-04239567.

XX

PA (MERE ) MERCK PATENT GMBH.

XX

PI Schubert P, Neumann S, Pawelzik M, Linxweiler W, Burger C;

PI Hofmann G, Bubert A, Goebel W, Koehler S;

XX

DR WPI; 1993-406956/51.

XX

PT New primers for PCR detection of Listeria - including individual species,  
PT also new peptide(s) for raising antibodies for immunochemical detection.

XX

PS Disclosure; Fig 2; 19pp; German.

XX

CC The sequence is that of a Listeria p60 peptide epitope which which may be  
CC used in the prodn. of antibodies for the detection of Listeria by  
CC immunoassay (partic. ELISA). It may be used as part of a method that  
CC allows determination of individual Listeria species, esp. L.  
CC monocytogenes. (Updated on 25-MAR-2003 to correct PN field.)

XX

SQ Sequence 11 AA;

Query Match 27.3%; Score 3; DB 2; Length 11;  
Best Local Similarity 100.0%; Pred. No. 7.9e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 AIK 11  
 |||  
Db 2 AIK 4

RESULT 21

AAR70606

ID AAR70606 standard; peptide; 11 AA.

XX

AC AAR70606;

XX

DT 14-FEB-1996 (first entry)

XX

DE HIV(B35)ARV2-7, human immunodeficiency virus epitope.

XX

KW HLA; human lymphocyte antigen; HIV; human immunodeficiency virus;

KW binding peptide; induce killer cell; prevention; treatment; AIDS;

KW autoimmune disease syndrome; vaccine.

XX

OS Human immunodeficiency virus.

XX

PN WO9511255-A1.

XX

PD 27-APR-1995.

XX

PF 19-OCT-1994; 94WO-JP001756.

XX

PR 19-OCT-1993; 93JP-00261302.

XX

PA (AJIN ) AJINOMOTO KK.

XX

PI Takiguchi M, Miwa K;

XX

DR WPI; 1995-170188/22.

XX

PT HLA-binding peptide fragments from HIV proteins - induce killer cells

PT which target HIV-infected cells and can be incorporated into anti-HIV

PT vaccines.

XX

PS Example 1; Page 10; 61pp; Japanese.

XX

CC AAR70606 is a peptide fragment derived from an HIV (Human

CC Immunodeficiency Virus) protein and is capable of binding to a human

CC lymphocyte antigen. The peptide can induce killer cells which target HIV-

CC infected cells. It is also useful in the prevention and treatment of HIV

CC and AIDS. Anti-HIV vaccines may incorporate the peptides, or may

CC incorporate a vector (such as vaccinia or BCG) contg. DNA encoding the

CC peptides

XX

SQ Sequence 11 AA;

Query Match 27.3%; Score 3; DB 2; Length 11;

Best Local Similarity 100.0%; Pred. No. 7.9e+03;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 RKS 4

Db

|||  
7 RKS 9

RESULT 22

AAR79902

ID AAR79902 standard; peptide; 11 AA.

XX

AC AAR79902;

XX

DT 19-MAR-1996 (first entry)

XX

DE Human FK-506 cytosolic binding protein FKBP12 residues 38-48.

XX

KW Human; cytosolic binding protein; FKBP12; residues 38-48; FK-506;

KW diagnosis; purification; determination; detection; immunosuppressant;

KW binding partner; antibodies.

XX

OS Homo sapiens.

XX

PN WO9521861-A1.

XX

PD 17-AUG-1995.

XX

PF 10-FEB-1995; 95WO-US001721.

XX

PR 15-FEB-1994; 94US-00197795.

XX

PA (MERI ) MERCK & CO INC.

XX

PI Wiederrecht GJ, Sewell TJ;

XX

DR WPI; 1995-293076/38.

XX

PT New FK-506 cytosolic binding protein - used for diagnostic, purification  
or investigational procedures, partic. for detection of FK-506.

XX

PS Disclosure; Page 9; 68pp; English.

XX

CC AAR79900-R79902 are peptides from the human FK-506 immunosuppressant  
CC cytosolic binding protein FKBP12. The peptides were conjugated to  
CC thyroglobulin, and used to generate anti-peptide antibodies. The  
CC antibodies were used to survey tissue and cell extracts relevant to the  
CC immunosuppressive effects FK-506. FKBP12 can be used as a specific  
CC binding partner for a variety of ligands for diagnostic, purifcn. and  
CC investigatory procedures. It can also be used to determine the presence  
CC or quantity of FK-506 in a sample, e.g. a body fluid from an  
CC immunosuppressed individual on FK-506 therapy

XX

SQ Sequence 11 AA;

Query Match 27.3%; Score 3; DB 2; Length 11;

Best Local Similarity 100.0%; Pred. No. 7.9e+03;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY

4 SRD 6

|||

## RESULT 23

AAR64598

ID AAR64598 standard; peptide; 11 AA.

XX

AC AAR64598;

XX

DT 25-MAR-2003 (revised)

DT 01-SEP-1995 (first entry)

XX

DE RF-1 peptide 43 from respiratory syncytial virus.

XX

KW antiviral activity; DP-178; DP-107; diagnostic; HIV-1LAI;

KW human immunodeficiency virus; transmembrane protein; gp41; alpha helix;

KW leucine zipper; DP-185; respiratory syncytial virus; RSV.

XX

OS Synthetic.

XX

FH Key Location/Qualifiers

FT Modified-site 1

FT /note= "optionally has an amino, acetyl, 9-

FT fluorenylmethoxy-carbonyl, hydrophobic or macromolecular

FT carrier gp. attached"

FT Modified-site 11

FT /note= "optionally has a carboxyl, amido, hydrophobic or

FT macromolecular carrier gp. attached"

XX

PN WO9428920-A1.

XX

PD 22-DEC-1994.

XX

PF 07-JUN-1994; 94WO-US005739.

XX

PR 07-JUN-1993; 93US-00073028.

XX

PA (UYDU-) UNIV DUKE.

XX

PI Bolognesi DP, Matthews TJ, Wild CT, Barney SO, Lambert DM;

PI Petteway SR;

XX

DR WPI; 1995-036105/05.

XX

PT Computer search generated synthetic peptides - are inhibitors of HIV  
PT transmission.

XX

PS Claim 14; Page 138; 182pp; English.

XX

CC AAR64591-623 are peptide derivatives of a 37 mer RF-1 peptide derived  
CC from respiratory syncytial virus (RSV) (AAR64590) which have been  
CC truncated at the amino terminus. The peptides are DP-178 like peptides.  
CC DP-178 corresponds to amino acids 638 to 673 of the HIV-1 isolate LAI  
CC transmembrane protein gp41. It forms a putative alpha helix at the C-  
CC terminal end of the gp41 ectodomain, and complexes with DP-107  
CC (corresponds to amino acids 558-595) which contains a leucine zipper  
CC motif. The peptides complex via non-covalent protein-protein



CC interactions. The peptide derivatives were identified by a computer  
CC assisted peptide sequence search. The antiviral activity of this peptide  
CC is not stated in the specification. (Updated on 25-MAR-2003 to correct PN  
CC field.)  
XX  
SQ Sequence 11 AA;

Query Match 27.3%; Score 3; DB 2; Length 11;  
Best Local Similarity 100.0%; Pred. No. 7.9e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 RKS 4  
|||  
Db 5 RKS 7

RESULT 24

AAR96813

ID AAR96813 standard; peptide; 11 AA.

XX

AC AAR96813;

XX

DT 29-NOV-1996 (first entry)

XX

DE Human laminin b2 fragment, homologous to N.gonorrhoeae MS11 IgaP.

XX

KW IgA protease precursor; IPP; bacterial polyprotein; autoimmune;

KW viral infection; rheumatoid arthritis; AIDS; meningococcal bacteria;

KW human laminin b2; Neisseria gonorrhoeae.

XX

OS Homo sapiens.

XX

FH Key Location/Qualifiers

FT Region 1. .5

FT /note= "identical to sequence in Neisseria gonorrhoeae  
FT IgaP"

FT Region 7

FT /note= "identical to corresponding residue in Neisseria  
FT gonorrhoeae IgaP"

FT Region 10. .11

FT /note= "identical to sequence in Neisseria gonorrhoeae  
FT IgaP"

XX

PN WO9609395-A2.

XX

PD 28-MAR-1996.

XX

PF 21-SEP-1995; 95WO-EP003726.

XX

PR 21-SEP-1994; 94DE-04433708.

XX

PA (PLAC ) MAX PLANCK GES FOERDERUNG WISSENSCHAFTEN.

XX

PI Meyer TF, Pohlner J, Beck SC, Jose J, Woelk U, Lorenzen DR;

PI Oetzelberger KB;

XX

DR WPI; 1996-188456/19.

XX  
PT Medicaments for treating auto-immune or viral diseases - contg.  
PT substances interfering with bacterial poly:protein function.  
XX  
PS Claim 32; Fig 2; 117pp; German.  
XX  
CC The present sequence from human laminin b2 has homology to a cleavage  
CC product from the IgaP domain of the precursor of IgA-protease polyprotein  
CC (IPP) of Neisseria gonorrhoeae strain MS11. The Neisseria IPP has been  
CC implicated in rheumatoid arthritis and other auto-immune diseases. The  
CC polyprotein also activates proviruses, including HIV. Substances which  
CC interfere with the function of IPP from Neisseria will be useful for  
CC treating associated autoimmune diseases and viral infections. Peptides  
CC comprising the homology region sequences, whether from Neisseria or from  
CC humans, are claimed  
XX  
SQ Sequence 11 AA;

Query Match 27.3%; Score 3; DB 2; Length 11;  
Best Local Similarity 100.0%; Pred. No. 7.9e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ARK 3  
|||  
Db 3 ARK 5

# RESULT 25

AAR96812

ID AAR96812 standard; peptide; 11 AA.

XX

AC AAR96812;

XX

DT 16-OCT-2003 (revised)

DT 29-NOV-1996 (first entry)

XX

DE N.gonorrhoeae MS11 IgaP region, homologous to human laminin b2.

XX

KW IgA protease precursor; IPP; bacterial polyprotein; autoimmune;

KW viral infection; rheumatoid arthritis; AIDS; meningococcal bacteria;

KW human laminin b2.

XX

OS Neisseria gonorrhoeae; MS11.

XX

FH Key Location/Qualifiers

FT Region 1. .5

FT /note= "identical to sequence in human laminin b2"

FT Region 7

FT /note= "identical to corresponding residue in human  
laminin b2"

FT Region 10. .11

FT /note= "identical to sequence in human laminin b2"

XX

PN W09609395-A2.

XX

PD 28-MAR-1996.

XX

PF 21-SEP-1995; 95WO-EP003726.  
 XX  
 PR 21-SEP-1994; 94DE-04433708.  
 XX  
 PA (PLAC ) MAX PLANCK GES FOERDERUNG WISSENSCHAFTEN.  
 XX  
 PI Meyer TF, Pohlner J, Beck SC, Jose J, Woelk U, Lorenzen DR;  
 PI Oetzelberger KB;  
 XX  
 DR WPI; 1996-188456/19.  
 XX  
 PT Medicaments for treating auto-immune or viral diseases - contg.  
 PT substances interfering with bacterial poly:protein function.  
 XX  
 PS Claim 32; Fig 2; 117pp; German.  
 XX  
 CC The present sequence is a cleavage product from the IgaP domain of the  
 CC precursor of IgA-protease polyprotein (IPP) of Neisseria gonorrhoeae  
 CC strain MS11. The Neisseria IPP has marked homology to certain human  
 CC proteins and has been implicated in rheumatoid arthritis and other auto-  
 CC immune diseases. The polyprotein also activates proviruses, including  
 CC HIV. Substances which interfere with the function of IPP from Neisseria  
 CC will be useful for treating associated autoimmune diseases and viral  
 CC infections. The present peptide is homologous to human laminin b2.  
 CC (Updated on 16-OCT-2003 to standardise OS field)  
 XX  
 SQ Sequence 11 AA;

Query Match 27.3%; Score 3; DB 2; Length 11;  
 Best Local Similarity 100.0%; Pred. No. 7.9e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ARK 3  
 |||  
 Db 3 ARK 5

# RESULT 26

AAR96834

ID AAR96834 standard; peptide; 11 AA.

XX

AC AAR96834;

XX

DT 16-OCT-2003 (revised)

DT 29-NOV-1996 (first entry)

XX

DE N.gonorrhoeae Iga alpha1 region, homologous to human Nfh protein.

XX

KW IgA protease precursor; IPP; bacterial polyprotein; autoimmune;

KW viral infection; rheumatoid arthritis; AIDS; meningococcal bacteria;

KW human neurofilament triplet h protein; Nfh.

XX

OS Neisseria gonorrhoeae; MS11.

XX

FH Key Location/Qualifiers

FT Region 1. .3

FT /note= "identical to sequence in human neurofilament

FT triplet h protein"  
 FT Region 5. .7  
 FT /note= "identical to sequence in human neurofilament  
 FT triplet h protein"  
 FT Region 10. .11  
 FT /note= "identical to sequence in human neurofilament  
 FT triplet h protein"  
 XX  
 PN WO9609395-A2.  
 XX  
 PD 28-MAR-1996.  
 XX  
 PF 21-SEP-1995; 95WO-EP003726.  
 XX  
 PR 21-SEP-1994; 94DE-04433708.  
 XX  
 PA (PLAC ) MAX PLANCK GES FOERDERUNG WISSENSCHAFTEN.  
 XX  
 PI Meyer TF, Pohlner J, Beck SC, Jose J, Woelk U, Lorenzen DR;  
 PI Oetzelberger KB;  
 XX  
 DR WPI; 1996-188456/19.  
 XX  
 PT Medicaments for treating auto-immune or viral diseases - contg.  
 PT substances interfering with bacterial poly:protein function.  
 XX  
 PS Claim 32; Fig 2; 117pp; German.  
 XX  
 CC The present sequence is a cleavage product from the Iga alpha 1 domain of  
 CC the precursor of IgA-protease polyprotein (IPP) of N.gonorrhoeae strain  
 CC MS11. The Neisseria IPP has marked homology to certain human proteins and  
 CC has been implicated in rheumatoid arthritis and other auto-immune  
 CC diseases. The polyprotein also activates proviruses, including HIV.  
 CC Substances which interfere with the function of IPP from Neisseria will  
 CC be useful for treating associated autoimmune diseases and viral  
 CC infections. The present peptide is homologous to a region from human  
 CC neurofilament triplet h protein. (Updated on 16-OCT-2003 to standardise  
 CC OS field)  
 XX  
 SQ Sequence 11 AA;

Query Match 27.3%; Score 3; DB 2; Length 11;  
 Best Local Similarity 100.0%; Pred. No. 7.9e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ARK 3  
 |||  
 Db 7 ARK 9

RESULT 27  
 AAW15309  
 ID AAW15309 standard; peptide; 11 AA.  
 XX  
 AC AAW15309;  
 XX  
 DT 01-JUL-1997 (first entry)

XX  
 DE 78 kDa glucose regulated protein.  
 XX  
 KW Release; expression; secretion; mammal; foetus; trophoblast; cell;  
 KW chorionic villus; unchanged; hypoxia; marker; indicator; abnormal;  
 KW maternal; placental; interface; function; abortion; screening;  
 KW intrauterine; growth; retardation; gestation; disease; tumour; molar;  
 KW pregnancy; choriocarcinoma; ectopic; apolipoprotein a-1; proteinuria;  
 KW hypertension; preeclampsia; induction; mitigation;  
 KW glucose regulated protein; 78 kDa; control.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO9633214-A2.  
 XX  
 PD 24-OCT-1996.  
 XX  
 PF 18-APR-1996; 96WO-US005441.  
 XX  
 PR 18-APR-1995; 95US-00423409.  
 XX  
 PA (REGC ) UNIV CALIFORNIA.  
 XX  
 PI Fisher SJ, Genbacev O, Foulk R, Clauser KR, Burlingame AL;  
 XX  
 DR WPI; 1996-497265/49.  
 XX  
 PT Detection of abnormal placental function or metastases - by detecting  
 PT proteins with altered expression or trophoblasts or chorionic villi under  
 PT hypoxic conditions.  
 XX  
 PS Example 2; Page 40; 57pp; English.  
 XX  
 CC The level of release of the present peptide by a mammalian foetal  
 CC trophoblast cell or a chorionic villus is unchanged when the cell or  
 CC villus is grown under hypoxic conditions, characterised by a partial  
 CC pressure of oxygen (pO2) of 14 mm Hg. The peptide can be used as a  
 CC control marker for the presence of hypoxic conditions indicative of an  
 CC abnormal maternal-placental interface, and consequent abnormal placental  
 CC function in, e.g. threatened abortion, intrauterine growth retardation,  
 CC gestational trophoblast diseases including molar pregnancy,  
 CC choriocarcinoma, placental site tumours, ectopic pregnancy, proteinuria,  
 CC pregnancy induced hypertension and preeclampsia. It can also be used as a  
 CC control in screens for inducers or mitigators of abnormal maternal-  
 CC placental interface  
 XX  
 SQ Sequence 11 AA;

Query Match 27.3%; Score 3; DB 2; Length 11;  
 Best Local Similarity 100.0%; Pred. No. 7.9e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 TAI 10  
 |||  
 Db 4 TAI 6

RESULT 28

AAW32498

ID AAW32498 standard; peptide; 11 AA.

XX

AC AAW32498;

XX

DT 21-APR-1998 (first entry)

XX

DE Helicostatin 9, which inhibits gut motility in the blowfly.

XX

KW Blowfly; callatostatin; insect neuropeptide; Leu-callatostatin;

KW gut motility; cockroach; insecticide; blowfly; cydiastatin; helicostatin.

XX

OS Helicoverpa armigera.

XX

PN WO9735981-A1.

XX

PD 02-OCT-1997.

XX

PF 26-MAR-1997; 97WO-GB000843.

XX

PR 26-MAR-1996; 96GB-00006272.

XX

PA (QUEE-) QUEEN MARY & WESTFIELD COLLEGE.

XX

PI Thorpe A, Duve H, Johnsen AH, East P;

XX

DR WPI; 1997-489644/45.

XX

PT New callatostatin-like peptide(s) and DNA - are active as inhibitors of  
PT gut motility, used as insecticides, particularly against lepidopteran  
PT insects.

XX

PS Claim 4; Page 63; 92pp; English.

XX

CC The present sequence represents a specifically claimed callatostatin-  
CC like peptide which is active as an inhibitor of gut motility. The  
CC callostatin-like peptides can be used as insecticides, particularly  
CC against lepidopteran insects. The invention relates to novel recombinant  
CC or isolated DNA sequences representing the Helicoverpa armigera  
CC helicostatin gene, the DraI fragment from Calliphora vomitoria or the  
CC Lucilia cuprina prohomone coding sequence. These sequences encode  
CC proteins of 228, 177 and 179 amino acids respectively

XX

SQ Sequence 11 AA;

Query Match 27.3%; Score 3; DB 2; Length 11;

Best Local Similarity 100.0%; Pred. No. 7.9e+03;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 RDM 7

|||

Db 2 RDM 4

RESULT 29

AAW41012

ID AAW41012 standard; peptide; 11 AA.  
 XX  
 AC AAW41012;  
 XX  
 DT 22-APR-1998 (first entry)  
 XX  
 DE Anti-glutathione antibody fragment VH1; DP-25.  
 XX  
 KW Antibody; glutathione; human; detection.  
 XX  
 OS Homo sapiens.  
 XX  
 PN JP09154583-A.  
 XX  
 PD 17-JUN-1997.  
 XX  
 PF 05-DEC-1995; 95JP-00316872.  
 XX  
 PR 05-DEC-1995; 95JP-00316872.  
 XX  
 PA (TANP-) TANPAKU KOGAKU KENKYUSHO KK.  
 XX  
 DR WPI; 1997-367063/34.  
 XX  
 PT Recombinant anti:glutathione antibody - useful for detection and  
 PT determination of glutathione.  
 XX  
 PS Claim 2; Page 10; 15pp; Japanese.  
 XX  
 CC This sequence represents a fragment of the antibody of the invention. The  
 CC antibody of the invention is an antibody which combines with glutathione  
 CC and with a protein modified by glutathione. The anti-glutathione antibody  
 CC is useful for detection and determination of glutathione  
 XX  
 SQ Sequence 11 AA;

Query Match 27.3%; Score 3; DB 2; Length 11;  
 Best Local Similarity 100.0%; Pred. No. 7.9e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 KSR 5  
 |||  
 Db 7 KSR 9

# RESULT 30

AAW40399

ID AAW40399 standard; protein; 11 AA.  
 XX  
 AC AAW40399;  
 XX  
 DT 17-OCT-2003 (revised)  
 DT 23-JUL-1998 (first entry)  
 XX  
 DE NNOS binding peptide #1.  
 XX  
 KW Nitric oxide synthase; endothelial; ENOS; INOS; inducible; NNOS;

KW neuronal; calmodulin; brain damage; shock; autoimmune disease;  
 KW inflammatory condition; multiple sclerosis; diabetes; dementia;  
 KW dysplasia; cancer; infectious disease; cytotoxic; hypertension;  
 KW atherosclerosis; asthma; detection; screening.  
 XX  
 OS unidentified.  
 XX  
 PN WO9802555-A1.  
 XX  
 PD 22-JAN-1998.  
 XX  
 PF 10-JUL-1997; 97WO-US012568.  
 XX  
 PR 12-JUL-1996; 96US-00679006.  
 XX  
 PA (SALE/) SALERNO J C.  
 XX  
 PI Salerno JC;  
 XX  
 DR WPI; 1998-110601/10.  
 XX  
 PT New modulators of nitric oxide synthase - used for treating e.g. toxic  
 PT shock, auto-immune disease, inflammatory disease, diabetes, hypertension,  
 PT infections or cancer.  
 XX  
 PS Claim 14; Page 41; 78pp; English.  
 XX  
 CC This sequence represents a peptide which binds adjacent to the calmodulin  
 CC binding site of neuronal nitric oxide synthase (NNOS). This peptide is  
 CC used in a novel method which identifies an agent which inhibits nitric  
 CC oxide synthase (NOS) by blocking calmodulin (CAM) activation of the NOS.  
 CC Such agents which modulate NOS activity can be used to treat a disease or  
 CC condition associated with nitric oxide production. Agents which inhibit  
 CC neuronal NOS (NNOS) can be used to prevent brain damage in conditions  
 CC involving cerebral ischaemia or reperfusion injury, such as head trauma.  
 CC Agents which decrease the activity of inducible NOS (INOS) can be used to  
 CC treat a condition modulated by production of NO by INOS, such as septic  
 CC shock, toxic shock, autoimmune disease such as rheumatoid arthritis,  
 CC inflammatory conditions such as inflammatory bowel disease, multiple  
 CC sclerosis, diabetes, or to combat dementia, immune system destruction,  
 CC and/or physical deterioration in individuals infected with the AIDS  
 CC virus. Agents which activate INOS can be used to treat disease relating  
 CC to dysplasia, cancer, or infectious disease. Activation of INOS can  
 CC produce cytotoxic levels of NO which would aid in the elimination of  
 CC dysplastic or cancerous tissue, or aid in the control of infectious  
 CC agents such as viruses, microbes, or other parasites. Agents which  
 CC increase the activity of endothelial NOS (ENOS) can be used to treat a  
 CC condition modulated by production of NO by ENOS such as hypertension,  
 CC atherosclerosis or acute asthma. An agent which activates ENOS or NNOS in  
 CC the corpus cavernosa can be used for treating male erectile dysfunction.  
 CC The products and methods can also be used for detection and drug  
 CC screening. (Updated on 17-OCT-2003 to standardise OS field)  
 XX  
 SQ Sequence 11 AA;

Query Match 27.3%; Score 3; DB 2; Length 11;  
 Best Local Similarity 100.0%; Pred. No. 7.9e+03;



Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 RKS 4  
|||  
Db 4 RKS 6

RESULT 31

AAW62282

ID AAW62282 standard; peptide; 11 AA.

XX

AC AAW62282;

XX

DT 24-SEP-1998 (first entry)

XX

DE Synthetic immunoglobulin TVG 405 light chain CDR3 peptide.

XX

KW HPV16; human papilloma virus; epithelial tumour; cervical cancer;

KW precancerous cervical lesion; screening; detection; infection; cervix;

KW HPV E4; immunoglobulin; antibody.

XX

OS Synthetic.

OS Human papillomavirus.

XX

PN WO9825145-A1.

XX

PD 11-JUN-1998.

XX

PF 03-DEC-1997; 97WO-GB003321.

XX

PR 03-DEC-1996; 96GB-00025142.

PR 05-SEP-1997; 97GB-00018745.

XX

PA (MEDI-) MEDICAL RES COUNCIL.

XX

PI Doorbar J;

XX

DR WPI; 1998-333497/29.

XX

PT Detecting papilloma virus infection using molecule binding to E4 protein

PT - useful, e.g. in screening for pre-cancerous cervical lesions and to

PT determine type(s) of human papilloma virus infecting human patients.

XX

PS Example 2; Page 17; 52pp; English.

XX

CC A new method has been developed for detecting a papilloma virus infection

CC in an organism. The method comprises: (i) obtaining a sample of cells

CC from the potential infection site; (ii) contacting the cells with a

CC molecule binding specifically to papilloma virus E4 protein, and (iii)

CC monitoring the binding. The method is useful to detect papilloma virus

CC infections in organisms (especially mammals) and especially HPV

CC infections (e.g. with HPV16, 18, 33, 35, 45, 51, 56, 58 or 61) in humans.

CC Papilloma viruses cause epithelial tumours in humans varying in severity

CC depending on the infection site and HPV type involved. The method is

CC particularly useful to determine papilloma infection in the mammalian

CC cervix and especially to screen for pre-cancerous cervical lesions in

CC humans, since over 90% of cervical carcinoma patients show cervical HPV

CC infection. It is also useful to determine the type(s) of HPV infection in  
CC a patient, by using a molecule binding specifically to a subset of HPV E4  
CC proteins. This is important, since progression to malignant disease (and  
CC hence clinical prognosis) is dependent on HPV type. Molecules capable of  
CC binding E4 are also useful to target anticancer/antiviral agents capable  
CC of destroying papilloma viruses and/or papilloma virus-infected cells.  
CC The present sequence represents a synthetic immunoglobulin TVG 405 light  
CC chain CDR3 peptide, from an example of the present invention

XX

SQ Sequence 11 AA;

Query Match 27.3%; Score 3; DB 2; Length 11;  
Best Local Similarity 100.0%; Pred. No. 7.9e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 SRD 6

|||

Db 2 SRD 4

RESULT 32

AAW41078

ID AAW41078 standard; peptide; 11 AA.

XX

AC AAW41078;

XX

DT 05-MAY-1998 (first entry)

XX

DE ADPHK protein sequence fragment, SEQ ID NO 3.

XX

KW ADPHK; enzyme; hexokinase; hexose 6-phosphate; adenosine 1-phosphate;

KW adenosine 2-phosphate; hexose.

XX

OS Synthetic.

XX

PN JP09327297-A.

XX

PD 22-DEC-1997.

XX

PF 12-MAR-1997; 97JP-00057330.

XX

PR 15-MAR-1996; 96JP-00059136.

XX

PA (ASAH ) ASAHI KASEI KOGYO KK.

XX

DR WPI; 1998-104115/10.

DR N-PSDB; AAV03982.

XX

PT DNA sequence encoding hexokinase - is used to transform organism for  
PT production of enzyme.

XX

PS Disclosure; Page 16; 17pp; Japanese.

XX

CC This sequence represents a fragment of the enzyme of the invention. The  
CC enzyme of the invention is designated ADPHK, and is a hexokinase. The DNA  
CC encoding this sequence was used to isolate the enzyme from P. furiosus or  
CC T. litoralis. The hexokinase of the invention is capable of catalysing

CC the formation of hexose 6-phosphate and adenosine 1-phosphate from  
CC adenosine 2-phosphate and hexose. The new DNA sequence is used to  
CC transform the microorganism which is capable of producing a hexokinase.  
CC The recombinant microorganism is highly efficient at producing the enzyme  
XX  
SQ Sequence 11 AA;

Query Match 27.3%; Score 3; DB 2; Length 11;  
Best Local Similarity 100.0%; Pred. No. 7.9e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 AIK 11  
|||  
Db 8 AIK 10

RESULT 33

AAW46000

ID AAW46000 standard; peptide; 11 AA.

XX

AC AAW46000;

XX

DT 03-JUL-1998 (first entry)

XX

DE Peptide #25 based on mouse SSTR 2 (residues 31-41).

XX

KW Hormone; receptor; antibody; vaccine; immunogen; somatostatin; IGF;

KW insulin-like growth factor binding protein; ILGFBP; SSTR; diabetes;

KW somatostatin receptor; insulin-like growth factor.

XX

OS Synthetic.

OS Mus sp.

XX

PN WO9744352-A1.

XX

PD 27-NOV-1997.

XX

PF 22-MAY-1997; 97WO-AU000312.

XX

PR 22-MAY-1996; 96AU-00009990.

XX

PA (NORT-) NORTHSTAR BIOLOGICALS PTY LTD.

XX

PI Gerraty NL, Westbrook SL, Kingston DJ;

XX

DR WPI; 1998-018427/02.

XX

PT New non-naturally occurring peptide(s) - which are based on portions of  
PT somatostatin, somatostatin receptors and insulin-like growth factor  
PT binding protein.

XX

PS Disclosure; Page 9; 136pp; English.

XX

CC Peptides AAW45983-W456025 are based on portions of somatostatin,  
CC somatostatin receptors (SSTR) and insulin-like growth factor binding  
CC proteins (IGFBP). They are capable of increasing weight gain, birth  
CC weight, growth rates, milk production, levels of circulating insulin, IGF

CC -I and IGF-III, fibre production and muscle weight. They may be used to  
CC modulate carbohydrate metabolism and in treatment of diabetes. The oil  
CC carrier may be used for delivery of the peptides  
XX  
SQ Sequence 11 AA;

Query Match 27.3%; Score 3; DB 2; Length 11;  
Best Local Similarity 100.0%; Pred. No. 7.9e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 DMT 8  
|||  
Db 7 DMT 9

RESULT 34

AAY20426

ID AAY20426 standard; protein; 11 AA.

XX

AC AAY20426;

XX

DT 22-JUL-1999 (first entry)

XX

DE Human microtubule associated protein 2 mutant fragment 122.

XX

KW Human; beta-amyloid precursor protein; beta-APP; diagnosis; cancer;  
KW frameshift mutation; age-related disease; neurodegenerative disorder;  
KW Alzheimer's disease; Down's syndrome; myotonic dystrophy; neuronal;  
KW Huntington's disease; multiple sclerosis; alcoholic liver disease;  
KW diabetes mellitus type II; microtubule associated protein; Tau; Big Tau;  
KW ubiquitin B; apolipoprotein E; MAP2; neurofilament-L; neurofilament-M;  
KW neurofilament-F; presenilin I; presenilin II; cellular tumour antigen;  
KW glial fibrillary acidic protein; GFAP; p53; semaphorin III; HUPF-1;  
KW bcl-2; B-cell leukemia/lymphoma 2 proto-oncogene; HMGP-C; NSP-A;  
KW high mobility group protein-C; neuroendocrine specific protein A.

XX

OS Synthetic.

OS Homo sapiens.

XX

PN W09845322-A2.

XX

PD 15-OCT-1998.

XX

PF 02-APR-1998; 98WO-IB000705.

XX

PR 10-APR-1997; 97US-0043163P.

XX

PA (ROYA-) ROYAL NETHERLANDS ACAD ARTS & SCI.

PA (UYRO-) UNIV ROTTERDAM ERASMUS.

PA (UYUT-) RIJKSUNIV UTRECHT.

XX

PI Van Leeuwen FW, Grosveld FG, Burbach JPH;

XX

DR WPI; 1998-609901/51.

DR N-PSDB; AAX75757.

XX

PT Diagnosing disease by detecting frameshift mutations in RNA or

PT corresponding protein mutations - used to diagnose cancer and  
PT neurological diseases, particularly Alzheimer's disease, and also for  
PT treatment and prevention with specific ribozymes or wild-type RNA.  
XX  
PS Disclosure; Fig 6; 258pp; English.  
XX  
CC This invention describes a novel method for the diagnosis of a disease  
CC caused by, or associated with, an RNA molecule that has a frameshift  
CC mutation. The method is used to diagnose age-related diseases, especially  
CC cancer and a wide range of neurodegenerative disorders (e.g. Alzheimer's  
CC disease, Down's syndrome, myotonic dystrophy, Huntington's disease,  
CC multiple sclerosis, alcoholic liver disease, diabetes mellitus type II  
CC and many others listed) or susceptibility to these disorders. The method  
CC allows a definitive diagnosis of Alzheimer's disease in living patients,  
CC at an early stage. It is based on the observation that disease may be  
CC caused by mutations in RNA rather than DNA. The invention describes the  
CC use of neuronal system RNA molecules, specifically proteins including  
CC beta-amyloid precursor protein (beta-APP), the microtubule associated  
CC proteins Tau and Big Tau, ubiquitin B, apolipoprotein E, microtubule  
CC associated protein 2 (MAP2), neurofilament-L, neurofilament-M,  
CC neurofilament-F, presenilin I, presenilin II, glial fibrillary acidic  
CC protein (GFAP), the cellular tumour antigen p53, B-cell leukemia/lymphoma  
CC 2 (bcl-2) proto-oncogene, semaphorin III, HUPF-1, high mobility group  
CC protein-C (HMGP-C) and neuroendocrine specific protein A  
XX  
SQ Sequence 11 AA;

Query Match 27.3%; Score 3; DB 2; Length 11;  
Best Local Similarity 100.0%; Pred. No. 7.9e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 RKS 4  
| | |  
Db 7 RKS 9

# RESULT 35

AAW61162

ID AAW61162 standard; peptide; 11 AA.

XX

AC AAW61162;

XX

DT 26-OCT-1998 (first entry)

XX

DE IgE derived oligopeptide 1.

XX

KW IgE Fc epsilon receptor; Cysteine; disulphide bond; loop structure;

KW anti-allergy treatment; anaphylactic immune response; antibody;

KW Type I hypersensitivity; hay fever; asthma.

XX

OS Homo sapiens.

XX

PN WO9824808-A2.

XX

PD 11-JUN-1998.

XX

PF 05-DEC-1997; 97WO-US022348.

XX  
 PR 06-DEC-1996; 96US-0031991P.  
 XX  
 PA (USSH ) US DEPT HEALTH & HUMAN SERVICES.  
 XX  
 PI Padlan EA, Birgit AH;  
 XX  
 DR WPI; 1998-333254/29.  
 XX  
 PT Oligopeptide interacting with human IgE Fc epsilon receptor - useful in  
 PT anti-allergy treatment as competitors of human IgE for Fc epsilon  
 PT receptor to block development of Type I hypersensitivity.  
 XX  
 PS Claim 1; Page 3; 45pp; English.  
 XX  
 CC The sequences AAW61162-W61166 are IgE derived oligopeptides which  
 CC interact with the human IgE Fc epsilon receptor. This particular  
 CC oligopeptide is the core minimal region of IgE required for interaction  
 CC with these Fc epsilon receptors and can thus bind both high and low  
 CC affinity receptors. The peptide was derived from a region of the epsilon  
 CC heavy chain of IgE, and can therefore mimic and block human IgE binding  
 CC to the Fc receptors. This sequence was used as the core sequence in the  
 CC other oligopeptides that were derived, they varied in length and at their  
 CC N and C terminal end. The IgE protein forms a loop structure naturally,  
 CC thus the addition of Cysteine residues at both ends of this sequence  
 CC enables disulphide bonds to form which results in a loop structure. These  
 CC oligopeptides are small and are thus easy to synthesise and deliver, they  
 CC are stable, highly active in anti-allergy treatment and lastly are less  
 CC likely to trigger an adverse anaphylatic immune response. The  
 CC oligopeptides can be used as competitors of human IgE for the Fc epsilon  
 CC receptor in anti-allergy treatment. Human IgE mediates Type I  
 CC hypersensitivity, an allergic response producing symptoms such as hay  
 CC fever and asthma. Thus the oligopeptides can be used to block the  
 CC development of type I hypersensitivity  
 XX  
 SQ Sequence 11 AA;

Query Match 27.3%; Score 3; DB 2; Length 11;  
 Best Local Similarity 100.0%; Pred. No. 7.9e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 RKS 4  
 |||  
 Db 9 RKS 11

# RESULT 36

AAY03092

ID AAY03092 standard; peptide; 11 AA.

XX

AC AAY03092;

XX

DT 08-JUN-1999 (first entry)

XX

DE New nociceptin analogue #74 from W09903880.

XX

KW Nociceptin; vasomotor disorder; menopausal hot flush; opioid antagonist;

KW hyperalgesia; neuroendocrine secretion; stress; locomotor activity;  
KW anxiety; instinctive behaviour; learning disorder; memory disorder;  
KW attention disorder; sensory perception disorder.  
XX  
OS Synthetic.  
XX  
FH Key Location/Qualifiers  
FT Modified-site 6. .10  
FT /note= "the side chains of residues 6 and 10 are  
FT condensed via a Gly residue to form a lactam bridge  
FT between these two positions"  
FT Modified-site 10  
FT /label= Orn  
FT /note= "ornithine residue"  
FT Modified-site 11  
FT /note= "C-terminal amide"  
XX  
PN WO9903880-A1.  
XX  
PD 28-JAN-1999.  
XX  
PF 13-JUL-1998; 98WO-DK000326.  
XX  
PR 15-JUL-1997; 97DK-00000867.  
PR 17-JUL-1997; 97US-0052862P.  
XX  
PA (NOVO ) NOVO-NORDISK AS.  
XX  
PI Thogersen H, Madsen K, Olsen UB, Johansen NL, Scheideler M;  
XX  
DR WPI; 1999-132156/11.  
XX  
PT New derivatives of nociceptin for treating vasomotor disorders -  
PT specifically hot flushes in menopausal women.  
XX  
PS Claim 70; Page 61; 69pp; English.  
XX  
CC This sequence is a specifically claimed example of new nociceptin  
CC analogue peptides which have the generic formula (X)n-A1-A2-A3-A4-A5- A6-  
CC A7-A8-A9-A10-A11-A12-A13-A14-A15-A16-A17-(Y)m-A18, in which: A1 is  
CC absent, a small or lipophilic amino acid, or phenylpropionic acid,  
CC optionally acylated; A2 = aromatic, lipophilic or small amino acid,  
CC optionally acylated if A1 is absent; A3, A6 and A7 = small, lipophilic or  
CC polar amino acids; A2-A3 may alternatively be 5-amino-pentanoic, N-  
CC methylantranilic, 4-aminocyclohexane carboxylic or 3-aminomethyl-  
CC benzoic acid; A4 = small, polar or aromatic amino acid; alternatively A3-  
CC A4 = N-methylantranilic acid; A5, A9, A10 and A11 = lipophilic or polar  
CC amino acids; A8 = polar amino acids or D- or L-Ala; A12, A13, A14 and A15  
CC = polar or lipophilic amino acids or may be absent; A16 and A17= small or  
CC polar amino acids or may be absent; A18 = hydroxy or amino; X and Y =  
CC polar, lipophilic, aromatic or small amino acids; n + m = 0-82; and two  
CC or more of A1-A17, X and Y may be cyclisation amino acids, forming one or  
CC more bridges (disulphide, lactam or Gly-lactam); provided that the  
CC peptide has (a) at least two amino acids modifications relative to the  
CC nociceptin sequence or (b) an unnatural amino acid at position A1. These  
CC peptides are useful for treatment and prevention of vasomotor disorders,  
CC specifically hot flushes in menopausal women. They can also be used for

CC antagonising the physiological effects of opioids and for treating  
CC diseases related to hyperalgesia, neuroendocrine secretion, stress,  
CC locomotor activity, anxiety, instinctive behaviour, and decrease in  
CC learning, memory, curiosity, attention and/or sensory perception  
XX  
SQ Sequence 11 AA;

Query Match 27.3%; Score 3; DB 2; Length 11;  
Best Local Similarity 100.0%; Pred. No. 7.9e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ARK 3  
|||  
Db 7 ARK 9

RESULT 37

AAY29752

ID AAY29752 standard; protein; 11 AA.

XX

AC AAY29752;

XX

DT 08-NOV-1999 (first entry)

XX

DE Modified HBc amino acid sequence fragment K79.

XX

KW Human hepatitis B core protein; HBc; modified; immunodominant;

KW nucleocapsid protein; vaccine; T cell epitope.

XX

OS Hepatitis B virus.

OS Synthetic.

XX

PN WO9940934-A1.

XX

PD 19-AUG-1999.

XX

PF 11-FEB-1999; 99WO-US003055.

XX

PR 12-FEB-1998; 98US-0074537P.

XX

PA (IMMU-) IMMUNE COMPLEX CORP.

XX

PI Birkett AJ;

XX

DR WPI; 1999-527340/44.

DR N-PSDB; AAZ08826.

XX

PT Conjugate of hepatitis B core protein, modified to increase reactivity  
PT with hapten, used to raise antibodies against the hapten, e.g. in  
PT vaccines.

XX

PS Example 6; Page 112; 128pp; English.

XX

CC The present invention describes a conjugate (A) comprising a  
CC strategically modified hepatitis B core (HBc) protein (I) attached to a  
CC hapten, where (I) includes amino acids (aa) 10-140 of the wild type HBc  
CC 183 aa sequence (given in AAY29674) and additionally has an insert (II)



CC in the region corresponding to aa's 50-100, where the insert is of 1 to  
CC about 40 aa's and contains a chemically reactive aa residue linked to the  
CC hapten. A vaccine containing (A), optionally in the form of particles, is  
CC used to induce a protective antibody response against the pathogen from  
CC which the hapten is derived, in humans or other animals. These pathogens  
CC may be bacteria, viruses, rickettsia or protozoa. Insertion of (II)  
CC overcomes the low reactivity of aa side chains in native HBc protein,  
CC increasing the reactivity with hapten and resulting in conjugates of  
CC improved immunogenicity. Modified HBc can be derivatised in the form of  
CC particles by well-defined chemical methods, and is unlikely to cause  
CC immunological side-effects. The present sequence represents a modified  
CC HBc fragment, having a lysine insertion, from the present invention

XX

SQ Sequence 11 AA;

Query Match 27.3%; Score 3; DB 2; Length 11;  
Best Local Similarity 100.0%; Pred. No. 7.9e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 SRD 6  
|||  
Db 8 SRD 10

RESULT 38

AAY47615

ID AAY47615 standard; peptide; 11 AA.

XX

AC AAY47615;

XX

DT 01-DEC-1999 (first entry)

XX

DE Immunogenic peptide having a human leukocyte antigen binding motif #2226.

XX

KW Human leukocyte antigen; binding; immunogenic; glycoprotein; MHC; HLA;  
KW immune response; T cell activation; major histocompatibility complex;  
KW cytotoxic T lymphocyte; CTL; tumour rejection; viral infection; cancer;  
KW prostate cancer; hepatitis B; hepatitis C; AIDS; renal carcinoma;  
KW vaccine; immunisation.

XX

OS Synthetic.

OS Homo sapiens.

XX

PN WO9945954-A1.

XX

PD 16-SEP-1999.

XX

PF 13-MAR-1998; 98WO-US005039.

XX

PR 13-MAR-1998; 98WO-US005039.

XX

PA (EPIM-) EPIMMUNE INC.

XX

PI Sette A, Kubo RT, Sidney J, Celis E, Grey HM, Southwood S;

XX

DR WPI; 1999-551214/46.

XX

PT New immunogenic peptides with HLA binding motif, useful in treatment and  
PT diagnosis of cancers and viral diseases.  
XX  
PS Claim 1; Page 116; 150pp; English.  
XX  
CC AAY45390 to AAY48214 represent specifically claimed immunogenic peptides  
CC having a human major histocompatibility complex (MHC) Class I (also known  
CC as human leukocyte antigen (HLA)) binding motif. The immunogenic peptides  
CC can bind to a specific HLA allele (i.e. HLA-A subtypes HLA-A2.1, A1, A3.2  
CC or A24.1 or HLA-B or C) and induce a cytotoxic T cell response against  
CC the antigen from which the peptide is derived. Cytotoxic T lymphocytes  
CC (CTLs) which destroy antigen-bearing cells are normally induced by an  
CC antigen in the form of a peptide fragment bound to a HLA molecule, rather  
CC than the intact foreign antigen itself, and are particularly important in  
CC tumour rejection and in fighting viral infections. The peptides are  
CC therefore useful therapeutically to treat or prevent viral infections and  
CC cancers in mammals (especially humans) e.g. prostate cancer, hepatitis B  
CC and C, AIDS, and renal carcinoma. They can be administered as vaccines to  
CC elicit an immune response in individuals susceptible or otherwise at risk  
CC of viral infection or cancer, or used to treat chronic or acute  
CC conditions. They are also useful diagnostically, and can be used to  
CC induce a cytotoxic T cell response, by contacting a cytotoxic T cell with  
CC the peptide e.g. to produce CTLs ex vivo for infusion back into a  
CC patient. The polynucleotides encoding the immunogenic peptides are also  
CC useful therapeutically and for immunisation as above  
XX  
SQ Sequence 11 AA;

Query Match 27.3%; Score 3; DB 2; Length 11;  
Best Local Similarity 100.0%; Pred. No. 7.9e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 TAI 10  
|||  
Db 6 TAI 8

# RESULT 39

AAW74077

ID AAW74077 standard; peptide; 11 AA.

XX

AC AAW74077;

XX

DT 04-MAY-1999 (first entry)

XX

DE Fragment of gastro-intestinal transport receptor binding peptide.

XX

KW Gastro-intestinal transport receptor; binding protein; hSI; HPT1; D2H;  
KW hPEPT1; human; GI tract receptor; sucrose-isomaltase complex;  
KW intestinal peptide-associated transporter; hypertension; diabetes;  
KW osteoporosis; haemophilia; anaemia; cancer; migraine; angina pectoris;  
KW therapeutic agent delivery; therapy.

XX

OS Homo sapiens.

XX

PN W09851325-A2.

XX

PD 19-NOV-1998.  
 XX  
 PF 15-MAY-1998; 98WO-US010088.  
 XX  
 PR 15-MAY-1997; 97US-0046595P.  
 XX  
 PA (CYTO-) CYTOGEN CORP.  
 PA (ELAN-) ELAN CORP PLC.  
 XX  
 PI Alvarez VL, Omahony DJ, Lambkin IJ, Patterson CA, Singleton J;  
 PI Belinka BA, Carter JM, Cagney GM;  
 XX  
 DR WPI; 1999-009568/01.  
 XX  
 PT New proteins that bind specifically to receptors in the gastro-intestinal  
 PT tract and related nucleic acid - chimaeras and antibodies, used to  
 PT deliver therapeutic or diagnostic agents to, or through, the  
 PT gastrointestinal tract, e.g. insulin or leuprolide.  
 XX  
 PS Claim 18; Page 236; 294pp; English.  
 XX  
 CC This sequence represents a fragment of a protien of the invention. The  
 CC invention relates to purified proteins (I) that bind specifically to at  
 CC least one of the gastro-intestinal (GI) tract receptors human intestinal  
 CC peptide-associated transporter (HPT1), hPEPT1, D2H and human sucrose-  
 CC isomaltase complex (hSI). (I) provide active transport of therapeutic  
 CC agents through human and animal GI tissue (into the blood) for in vivo  
 CC delivery, particularly for treatment or prevention of hypertension,  
 CC diabetes, osteoporosis, haemophilia, anaemia, cancer, migraine, or angina  
 CC pectoris. Specifically they are used to deliver insulin or leuprolide,  
 CC but many other suitable therapeutic agents are disclosed, including genes  
 CC or inhibitory nucleic acid, imaging agents and antigens. (I) may also  
 CC provide targeting to the GI tract. Other uses of (I) are: (i) to  
 CC determine the level of specified receptors in a sample (in a binding  
 CC assay); and (ii) to screen for molecules that bind (I). Immunogenic  
 CC analogues or derivatives of (I) are used to raise antibodies and in  
 CC immunoassays. The antibodies are used to locate, detect and measure (I),  
 CC e.g. for imaging, monitoring treatment, tissue analysis etc., also for  
 CC peptide purification and immobilisation  
 XX  
 SQ Sequence 11 AA;

Query Match 27.3%; Score 3; DB 2; Length 11;  
 Best Local Similarity 100.0%; Pred. No. 7.9e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 RKS 4  
 |||  
 Db 3 RKS 5

RESULT 40  
 AAW74135  
 ID AAW74135 standard; peptide; 11 AA.  
 XX  
 AC AAW74135;  
 XX

DT 04-MAY-1999 (first entry)  
 XX  
 DE GI transport receptor binding protein fragment.  
 XX  
 KW Gastro-intestinal transport receptor; binding protein; hSI; HPT1; D2H;  
 KW hPEPT1; human; GI tract receptor; sucrose-isomaltase complex;  
 KW intestinal peptide-associated transporter; hypertension; diabetes;  
 KW osteoporosis; haemophilia; anaemia; cancer; migraine; angina pectoris;  
 KW therapeutic agent delivery; therapy; fusion protein.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO9851325-A2.  
 XX  
 PD 19-NOV-1998.  
 XX  
 PF 15-MAY-1998; 98WO-US010088.  
 XX  
 PR 15-MAY-1997; 97US-0046595P.  
 XX  
 PA (CYTO-) CYTOGEN CORP.  
 PA (ELAN-) ELAN CORP PLC.  
 XX  
 PI Alvarez VL, Omahony DJ, Lambkin IJ, Patterson CA, Singleton J;  
 PI Belinka BA, Carter JM, Cagney GM;  
 XX  
 DR WPI; 1999-009568/01.  
 XX  
 PT New proteins that bind specifically to receptors in the gastro-intestinal  
 PT tract and related nucleic acid - chimaeras and antibodies, used to  
 PT deliver therapeutic or diagnostic agents to, or through, the  
 PT gastrointestinal tract, e.g. insulin or leuprolide.  
 XX  
 PS Disclosure; Page 195; 294pp; English.  
 XX  
 CC This sequence represents a fragment of a gastro-intestinal transport  
 CC protein binding peptide. The invention relates to purified proteins (I)  
 CC that bind specifically to at least one of the gastro-intestinal (GI)  
 CC tract receptors human intestinal peptide-associated transporter (HPT1),  
 CC hPEPT1, D2H and human sucrose-isomaltase complex (hSI). (I) provide  
 CC active transport of therapeutic agents through human and animal GI tissue  
 CC (into the blood) for in vivo delivery, particularly for treatment or  
 CC prevention of hypertension, diabetes, osteoporosis, haemophilia, anaemia,  
 CC cancer, migraine, or angina pectoris. Specifically they are used to  
 CC deliver insulin or leuprolide, but many other suitable therapeutic agents  
 CC are disclosed, including genes or inhibitory nucleic acid, imaging agents  
 CC and antigens. (I) may also provide targeting to the GI tract. Other uses  
 CC of (I) are: (i) to determine the level of specified receptors in a sample  
 CC (in a binding assay); and (ii) to screen for molecules that bind (I).  
 CC Immunogenic analogues or derivatives of (I) are used to raise antibodies  
 CC and in immunoassays. The antibodies are used to locate, detect and  
 CC measure (I), e.g. for imaging, monitoring treatment, tissue analysis  
 CC etc., also for peptide purification and immobilisation  
 XX  
 SQ Sequence 11 AA;

Query Match

27.3%; Score 3; DB 2; Length 11;

Best Local Similarity 100.0%; Pred. No. 7.9e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 RKS 4  
|||  
Db 2 RKS 4

RESULT 41

AAW97473

ID AAW97473 standard; peptide; 11 AA.

XX

AC AAW97473;

XX

DT 19-MAY-1999 (first entry)

XX

DE Antigenic site of HN protein loop beta-2L01.

XX

KW Antigenic site; haemagglutinin-neuraminidase; HN; paramyxoviridae;  
KW virus epitope; attachment protein; vaccine; immunodominant epitope.

XX

OS Sendai virus.

XX

PN WO9902695-A2.

XX

PD 21-JAN-1999.

XX

PF 08-JUL-1998; 98WO-NL000390.

XX

PR 08-JUL-1997; 97EP-00202100.

XX

PA (DIER-) STICHTING INST DIERHOUDERIJ EN DIERGEZON.

XX

PI Langedijk JPM, Van Oirschot JT;

XX

DR WPI; 1999-120896/10.

XX

PT Isolated proteinaceous substance - comprising at least one virus epitope  
PT derived from an attachment protein of a paramyxovirus.

XX

PS Disclosure; Page 43; 63pp; English.

XX

CC AAW97452-571 represent antigenic sites derived from the haemagglutinin-  
CC neuraminidase (HN) protein of the paramyxoviridae. The specification  
CC describes 3-D models identifying a proteinaceous substance comprising at  
CC least one virus epitope derived from the attachment protein, which  
CC corresponds to an antigenic site present on one of the loops of HN. The  
CC antigenic sites can be used to produce vaccines, to detect the viruses,  
CC and to select the immunodominant epitope

XX

SQ Sequence 11 AA;

Query Match 27.3%; Score 3; DB 2; Length 11;

Best Local Similarity 100.0%; Pred. No. 7.9e+03;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 RKS 4

|||

Db               9 RKS 11

RESULT 42

ID    AAW97472 standard; peptide; 11 AA.

AC AAW97472;

DT 19-MAY-1999 (first entry)

DE Antigenic site of HN protein loop beta-2L01.

KW Antigenic site; haemagglutinin-neuraminidase; HN; paramyxoviridae;  
KW virus epitope; attachment protein; vaccine; immunodominant epitope.

OS Bovine parainfluenza virus.

PN WO9902695-A2.

PD 21-JAN-1999.

PF 08-JUL-1998; 98WO-NL000390.

PR 08-JUL-1997; 97EP-00202100.

PA (DIER-) STICHTING INST DIERHOUDERIJ EN DIERGEZON.

PI Langedijk JPM, Van Oirschot JT;

DR WPI; 1999-120896/10.

PT Isolated proteinaceous substance - comprising at least one virus epitope  
PT derived from an attachment protein of a paramyxovirus.

PS Disclosure; Page 43; 63pp; English.

AAW97452-571 represent antigenic sites derived from the haemagglutinin-neuraminidase (HN) protein of the paramyxoviridae. The specification describes 3-D models identifying a proteinaceous substance comprising at least one virus epitope derived from the attachment protein, which corresponds to an antigenic site present on one of the loops of HN. The antigenic sites can be used to produce vaccines, to detect the viruses, and to select the immunodominant epitope

SQ Sequence 11 AA;

Query Match 27.3%; Score 3; DB 2; Length 11;

Best Local Similarity 100.0%; Pred. No. 7.9e+03;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 RKS 4

111

Db 9 RKS 11

RESULT 43

AAW97476

ID AAW97476 standard; peptide; 11 AA.

XX

AC AAW97476;

XX

DT 19-MAY-1999 (first entry)

XX

DE Antigenic site of HN protein loop beta-2L01.

XX

KW Antigenic site; haemagglutinin-neuraminidase; HN; paramyxoviridae;  
KW virus epitope; attachment protein; vaccine; immunodominant epitope.

XX

OS Mumps virus.

XX

PN WO9902695-A2.

XX

PD 21-JAN-1999.

XX

PF 08-JUL-1998; 98WO-NL000390.

XX

PR 08-JUL-1997; 97EP-00202100.

XX

PA (DIER-) STICHTING INST DIERHOUDERIJ EN DIERGEZON.

XX

PI Langedijk JPM, Van Oirschot JT;

XX

DR WPI; 1999-120896/10.

XX

PT Isolated proteinaceous substance - comprising at least one virus epitope  
PT derived from an attachment protein of a paramyxovirus.

XX

PS Disclosure; Page 43; 63pp; English.

XX

CC AAW97452-571 represent antigenic sites derived from the haemagglutinin-  
CC neuraminidase (HN) protein of the paramyxoviridae. The specification  
CC describes 3-D models identifying a proteinaceous substance comprising at  
CC least one virus epitope derived from the attachment protein, which  
CC corresponds to an antigenic site present on one of the loops of HN. The  
CC antigenic sites can be used to produce vaccines, to detect the viruses,  
CC and to select the immunodominant epitope

XX

SQ Sequence 11 AA;

Query Match 27.3%; Score 3; DB 2; Length 11;

Best Local Similarity 100.0%; Pred. No. 7.9e+03;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 RKS 4

|||

Db 9 RKS 11

RESULT 44

AAW97477

ID AAW97477 standard; peptide; 11 AA.

XX

AC AAW97477;  
 XX  
 DT 19-MAY-1999 (first entry)  
 XX  
 DE Antigenic site of HN protein loop beta-2L01.  
 XX  
 KW Antigenic site; haemagglutinin-neuraminidase; HN; paramyxoviridae;  
 KW virus epitope; attachment protein; vaccine; immunodominant epitope.  
 XX  
 OS Newcastle disease virus.  
 XX  
 PN W09902695-A2.  
 XX  
 PD 21-JAN-1999.  
 XX  
 PF 08-JUL-1998; 98WO-NL000390.  
 XX  
 PR 08-JUL-1997; 97EP-00202100.  
 XX  
 PA (DIER-) STICHTING INST DIERHOUDERIJ EN DIERGEZON.  
 XX  
 PI Langedijk JPM, Van Oirschot JT;  
 XX  
 DR WPI; 1999-120896/10.  
 XX  
 PT Isolated proteinaceous substance - comprising at least one virus epitope  
 PT derived from an attachment protein of a paramyxovirus.  
 XX  
 PS Disclosure; Page 43; 63pp; English.  
 XX  
 CC AAW97452-571 represent antigenic sites derived from the haemagglutinin-  
 CC neuraminidase (HN) protein of the paramyxoviridae. The specification  
 CC describes 3-D models identifying a proteinaceous substance comprising at  
 CC least one virus epitope derived from the attachment protein, which  
 CC corresponds to an antigenic site present on one of the loops of HN. The  
 CC antigenic sites can be used to produce vaccines, to detect the viruses,  
 CC and to select the immunodominant epitope  
 XX  
 SQ Sequence 11 AA;

Query Match 27.3%; Score 3; DB 2; Length 11;  
 Best Local Similarity 100.0%; Pred. No. 7.9e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 RKS 4  
 |||  
 Db 9 RKS 11

RESULT 45  
 AAW97474  
 ID AAW97474 standard; peptide; 11 AA.  
 XX  
 AC AAW97474;  
 XX  
 DT 19-MAY-1999 (first entry)  
 XX



DE Antigenic site of HN protein loop beta-2L01.  
 XX  
 KW Antigenic site; haemagglutinin-neuraminidase; HN; paramyxoviridae;  
 KW virus epitope; attachment protein; vaccine; immunodominant epitope.  
 XX  
 OS Human parainfluenza virus.  
 XX  
 PN WO9902695-A2.  
 XX  
 PD 21-JAN-1999.  
 XX  
 PF 08-JUL-1998; 98WO-NL000390.  
 XX  
 PR 08-JUL-1997; 97EP-00202100.  
 XX  
 PA (DIER-) STICHTING INST DIERHOUDERIJ EN DIERGEZON.  
 XX  
 PI Langedijk JPM, Van Oirschot JT;  
 XX  
 DR WPI; 1999-120896/10.  
 XX  
 PT Isolated proteinaceous substance - comprising at least one virus epitope  
 PT derived from an attachment protein of a paramyxovirus.  
 XX  
 PS Disclosure; Page 43; 63pp; English.  
 XX  
 CC AAW97452-571 represent antigenic sites derived from the haemagglutinin-  
 CC neuraminidase (HN) protein of the paramyxoviridae. The specification  
 CC describes 3-D models identifying a proteinaceous substance comprising at  
 CC least one virus epitope derived from the attachment protein, which  
 CC corresponds to an antigenic site present on one of the loops of HN. The  
 CC antigenic sites can be used to produce vaccines, to detect the viruses,  
 CC and to select the immunodominant epitope  
 XX  
 SQ Sequence 11 AA;

Query Match 27.3%; Score 3; DB 2; Length 11;  
 Best Local Similarity 100.0%; Pred. No. 7.9e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 RKS 4  
 |||  
 Db 9 RKS 11

RESULT 46

AAW97475

ID AAW97475 standard; peptide; 11 AA.

XX

AC AAW97475;

XX

DT 27-AUG-2003 (revised)

DT 19-MAY-1999 (first entry)

XX

DE Antigenic site of HN protein loop beta-2L01.

XX

KW Antigenic site; haemagglutinin-neuraminidase; HN; paramyxoviridae;

KW virus epitope; attachment protein; vaccine; immunodominant epitope.  
 XX  
 OS Unidentified.  
 XX  
 PN WO9902695-A2.  
 XX  
 PD 21-JAN-1999.  
 XX  
 PF 08-JUL-1998; 98WO-NL000390.  
 XX  
 PR 08-JUL-1997; 97EP-00202100.  
 XX  
 PA (DIER-) STICHTING INST DIERHOUDERIJ EN DIERGEZON.  
 XX  
 PI Langedijk JPM, Van Oirschot JT;  
 XX  
 DR WPI; 1999-120896/10.  
 XX  
 PT Isolated proteinaceous substance - comprising at least one virus epitope  
 PT derived from an attachment protein of a paramyxovirus.  
 XX  
 PS Disclosure; Page 43; 63pp; English.  
 XX  
 CC AAW97452-571 represent antigenic sites derived from the haemagglutinin-  
 CC neuraminidase (HN) protein of the paramyxoviridae. The specification  
 CC describes 3-D models identifying a proteinaceous substance comprising at  
 CC least one virus epitope derived from the attachment protein, which  
 CC corresponds to an antigenic site present on one of the loops of HN. The  
 CC antigenic sites can be used to produce vaccines, to detect the viruses,  
 CC and to select the immunodominant epitope. (Updated on 27-AUG-2003 to  
 CC correct OS field.)  
 XX  
 SQ Sequence 11 AA;

Query Match 27.3%; Score 3; DB 2; Length 11;  
 Best Local Similarity 100.0%; Pred. No. 7.9e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 RKS 4  
 |||  
 Db 9 RKS 11

#### RESULT 47

AAAY02916

ID AAY02916 standard; protein; 11 AA.  
 XX  
 AC AAY02916;  
 XX  
 DT 11-JUN-1999 (first entry)  
 XX  
 DE Fragment of human secreted protein encoded by gene 98.  
 XX  
 KW Human; secreted protein; fusion protein; gene therapy; protein therapy;  
 KW diagnosis; tissue; cancer; tumour; neurodegenerative disorder; leukaemia;  
 KW developmental abnormality; foetal deficiency; blood; allergy; renal;  
 KW immune system; asthma; lymphocytic disease; brain; hepatic; lymphoma;

KW inflammation; ischaemic shock; Alzheimer's disease; restenosis; AIDS;  
 KW cognitive disorder; schizophrenia; prostate; obesity; osteoclast; thymus;  
 KW osteoporosis; arthritis; testis; lung; thyroiditis; thyroid; digestion;  
 KW endocrine; metabolism; regulation; malabsorption; gastritis; neoplasm.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO9902546-A1.  
 XX  
 PD 21-JAN-1999.  
 XX  
 PF 07-JUL-1998; 98WO-US013684.  
 XX  
 PR 08-JUL-1997; 97US-0051916P.  
 PR 08-JUL-1997; 97US-0051918P.  
 PR 08-JUL-1997; 97US-0051919P.  
 PR 08-JUL-1997; 97US-0051920P.  
 PR 08-JUL-1997; 97US-0051925P.  
 PR 08-JUL-1997; 97US-0051926P.  
 PR 08-JUL-1997; 97US-0051928P.  
 PR 08-JUL-1997; 97US-0051929P.  
 PR 08-JUL-1997; 97US-0051930P.  
 PR 08-JUL-1997; 97US-0051931P.  
 PR 08-JUL-1997; 97US-0051932P.  
 PR 08-JUL-1997; 97US-0052732P.  
 PR 08-JUL-1997; 97US-0052733P.  
 PR 08-JUL-1997; 97US-0052793P.  
 PR 08-JUL-1997; 97US-0052795P.  
 PR 08-JUL-1997; 97US-0052803P.  
 PR 18-AUG-1997; 97US-0055684P.  
 PR 18-AUG-1997; 97US-0055722P.  
 PR 18-AUG-1997; 97US-0055723P.  
 PR 18-AUG-1997; 97US-0055947P.  
 PR 18-AUG-1997; 97US-0055948P.  
 PR 18-AUG-1997; 97US-0055949P.  
 PR 18-AUG-1997; 97US-0055950P.  
 PR 18-AUG-1997; 97US-0055953P.  
 PR 18-AUG-1997; 97US-0055954P.  
 PR 18-AUG-1997; 97US-0055964P.  
 PR 18-AUG-1997; 97US-0055984P.  
 PR 18-AUG-1997; 97US-0056360P.  
 PR 12-SEP-1997; 97US-0058660P.  
 PR 12-SEP-1997; 97US-0058661P.  
 PR 12-SEP-1997; 97US-0058664P.  
 PR 12-SEP-1997; 97US-0058785P.  
 XX  
 PA (HUMA-) HUMAN GENOME SCI INC.  
 XX  
 PI Fischer CL, Rosen CA, Soppet DR, Ruben SM, Kyaw H, Li Y, Zeng Z;  
 PI Lafleur DW, Moore PA, Shi Y, Olsen HS, Ebner R, Brewer LA;  
 XX  
 DR WPI; 1999-120770/10.  
 XX  
 PT New isolated human genes and the secreted polypeptides they encode -  
 PT useful for diagnosis and treatment of e.g. cancers, neurological  
 PT disorders, immune diseases, inflammation or blood disorders.  
 XX

PS Disclosure; Page 115; 464pp; English.

XX

CC This sequence represents a fragment of a secreted human protein encoded  
CC by the nucleic acid molecule detailed in the descriptor line. The gene  
CC can be used to generate fusion proteins by linking to the gene to a human  
CC immunoglobulin Fc portion (e.g. AAX27302) for increasing the stability of  
CC the fused protein as compared to the human protein only. The invention  
CC relates to 123 novel genes and their fragments (nucleic acid sequences:  
CC AAX27311-X27449; amino acid sequences AAY02650-Y02788) which are useful  
CC for preventing, treating or ameliorating medical conditions e.g. by  
CC protein or gene therapy. Also, pathological conditions can be diagnosed  
CC by determining the amount of the new polypeptides in a sample or by  
CC determining the presence of mutations in the new polynucleotides.  
CC Specific uses are described for each of the 123 polynucleotides, based on  
CC which tissues they are most highly expressed in (see AAX27311 for  
CC described uses)

XX

SQ Sequence 11 AA;

Query Match 27.3%; Score 3; DB 2; Length 11;

Best Local Similarity 100.0%; Pred. No. 7.9e+03;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 AIK 11

|||

Db 7 AIK 9

#### RESULT 48

AAY89315

ID AAY89315 standard; peptide; 11 AA.

XX

AC AAY89315;

XX

DT 23-MAY-2000 (first entry)

XX

DE Core polypeptide fragment T No. 821.

XX

KW Retrovirus; hybrid polypeptide; enhancer; gp41; envelope protein; HIV-1;

KW HIV-2; SIV; pharmacokinetic; half-life; growth factor; cytokine; viral;

KW anti-fusogenic; differentiation factor; interleukin; interferon;

KW colony stimulating factor; hormone; angiogenic factor.

XX

OS Unidentified.

XX

PN WO9959615-A1.

XX

PD 25-NOV-1999.

XX

PF 20-MAY-1999; 99WO-US011219.

XX

PR 20-MAY-1998; 98US-00082279.

XX

PA (TRIM-) TRIMERIS INC.

XX

PI Barney S, Guthrie KI, Merutka G, Anwer MK, Lambert DM;

XX

DR WPI; 2000-136792/12.  
XX  
PT A new hybrid polypeptide with enhanced pharmacokinetic properties  
PT comprises enhancer sequence.  
XX  
PS Disclosure; Page 34; 124pp; English.  
XX  
CC The invention relates to hybrid polypeptides comprising enhancer peptide  
CC sequence linked to core polypeptides. The enhancer polypeptides are  
CC derived from various retroviral envelope (gp41) protein sequences,  
CC especially from HIV-1, HIV-2 and SIV. The enhancer peptides enhance the  
CC pharmacokinetic properties such as increasing the half-life of any core  
CC polypeptide that they are linked to. The core polypeptides are any  
CC polypeptide that may be introduced into a living system and that can  
CC function as a pharmacologically useful peptide for the treatment or  
CC prevention of a disease. The core polypeptides are bioactive peptides  
CC selected from a growth factor, cytokine, differentiation factor,  
CC interleukin, interferon, colony stimulating factor, hormone or angiogenic  
CC factor. The peptides of the invention can be used for inhibiting viral  
CC infection and can be used in anti-viral and anti-fusogenic treatments.  
CC Sequences AAY88651-Y90055 represent core polypeptide fragments that can  
CC be used in the invention. Some sequences among those indicated also  
CC comprise enhancer fragments at terminal ends and form hybrid polypeptides  
XX  
SQ Sequence 11 AA;

Query Match 27.3%; Score 3; DB 3; Length 11;  
Best Local Similarity 100.0%; Pred. No. 7.9e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 RKS 4  
|||  
Db 4 RKS 6

RESULT 49

AAY81922

ID AAY81922 standard; peptide; 11 AA.

XX

AC AAY81922;

XX

DT 23-JUN-2000 (first entry)

XX

DE Asparagine protease recognition peptide.

XX

KW Asparagine protease recognition peptide; protease assay; enzyme cleavage;  
KW plant protease.

XX

OS Glycine max.

XX

PN JP3015886-B1.

XX

PD 06-MAR-2000.

XX

PF 04-NOV-1998; 98JP-00327536.

XX

PR 04-NOV-1998; 98JP-00327536.

XX  
PA (NORQ ) NORINSUISANSHO SHOKUHIN SOGO.  
XX  
DR WPI; 2000-342275/30.  
XX  
PT Quick assay method of specific end protease activity of asparagine  
PT residue of plant origin, involves distributing 7-methoxy phosphorous 4-yl  
PT -acetyl and 2,4-dinitrophenyl group to N-terminal side and C-terminal  
PT side.  
XX  
PS Example 2; Page 9; 11pp; Japanese.  
XX  
CC This sequence represents a peptide recognised and cleaved by asparagine  
CC protease. The invention relates to a quick assay method for asparagine  
CC protease of plant origin. The asparagine protease specifically recognises  
CC asparagine residues and cleaves proteins at the C-terminal end of the  
CC asparagine residue. The assay uses a fluorescence substrate (which has  
CC quenching properties) which distributes a 7-methoxy coumarin-4-yl-acetyl  
CC group to the amino group of the glycine residue at the N-terminal side,  
CC and a 2,4-dinitrophenyl group to the C-terminal of an amino acid  
CC sequence. The fluorescence caused by the fluorescence substrate is not  
CC connected to the asparagine residue and can be measured after cleavage by  
CC the protease. The method is useful for assaying asparagine proteases of  
CC plant origin. The activity of the protease can be determined within a  
CC short time period and the enzyme activity can be measured with high  
CC sensitivity using the fluorescence substrate. The procedure is quick even  
CC when materials which inhibit other protease and fluorescence are included  
CC in the sample  
XX  
SQ Sequence 11 AA;

Query Match 27.3%; Score 3; DB 3; Length 11;  
Best Local Similarity 100.0%; Pred. No. 7.9e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 KSR 5  
| | |  
Db 2 KSR 4

RESULT 50  
AAY81923  
ID AAY81923 standard; peptide; 11 AA.  
XX  
AC AAY81923;  
XX  
DT 23-JUN-2000 (first entry)  
XX  
DE Asparagine protease recognition peptide.  
XX  
KW Asparagine protease recognition peptide; protease assay; enzyme cleavage;  
KW plant protease.  
XX  
OS Glycine max.  
XX  
PN JP3015886-B1.  
XX

PD 06-MAR-2000.  
 XX  
 PF 04-NOV-1998; 98JP-00327536.  
 XX  
 PR 04-NOV-1998; 98JP-00327536.  
 XX  
 PA (NORQ ) NORINSUISANSHO SHOKUHIN SOGO.  
 XX  
 DR WPI; 2000-342275/30.  
 XX  
 PT Quick assay method of specific end protease activity of asparagine  
 PT residue of plant origin, involves distributing 7-methoxy phosphorous 4-yl  
 PT -acetyl and 2,4-dinitrophenyl group to N-terminal side and C-terminal  
 PT side.  
 XX  
 PS Example 2; Page 9; 11pp; Japanese.  
 XX  
 CC This sequence represents a peptide recognised and cleaved by asparagine  
 CC protease. The invention relates to a quick assay method for asparagine  
 CC protease of plant origin. The asparagine protease specifically recognises  
 CC asparagine residues and cleaves proteins at the C-terminal end of the  
 CC asparagine residue. The assay uses a fluorescence substrate (which has  
 CC quenching properties) which distributes a 7-methoxy coumarin-4-yl-acetyl  
 CC group to the amino group of the glycine residue at the N-terminal side,  
 CC and a 2,4-dinitrophenyl group to the C-terminal of an amino acid  
 CC sequence. The fluorescence caused by the fluorescence substrate is not  
 CC connected to the asparagine residue and can be measured after cleavage by  
 CC the protease. The method is useful for assaying asparagine proteases of  
 CC plant origin. The activity of the protease can be determined within a  
 CC short time period and the enzyme activity can be measured with high  
 CC sensitivity using the fluorescence substrate. The procedure is quick even  
 CC when materials which inhibit other protease and fluorescence are included  
 CC in the sample  
 XX  
 SQ Sequence 11 AA;

Query Match 27.3%; Score 3; DB 3; Length 11;  
 Best Local Similarity 100.0%; Pred. No. 7.9e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 KSR 5  
 |||  
 Db 2 KSR 4

# RESULT 51

AAY81915

ID AAY81915 standard; peptide; 11 AA.

XX

AC AAY81915;

XX

DT 23-JUN-2000 (first entry)

XX

DE Asparagine protease recognition peptide.

XX

KW Asparagine protease recognition peptide; protease assay; enzyme cleavage;  
 KW plant protease.

XX  
 OS Glycine max.  
 XX  
 PN JP3015886-B1.  
 XX  
 PD 06-MAR-2000.  
 XX  
 PF 04-NOV-1998; 98JP-00327536.  
 XX  
 PR 04-NOV-1998; 98JP-00327536.  
 XX  
 PA (NORQ ) NORINSUISANSHO SHOKUHN SOGO.  
 XX  
 DR WPI; 2000-342275/30.  
 XX  
 PT Quick assay method of specific end protease activity of asparagine  
 PT residue of plant origin, involves distributing 7-methoxy phosphorous 4-yl  
 PT -acetyl and 2,4-dinitrophenyl group to N-terminal side and C-terminal  
 PT side.  
 XX  
 PS Claim 1; Page 8; 11pp; Japanese.  
 XX  
 CC This sequence represents a peptide recognised and cleaved by asparagine  
 CC protease. The invention relates to a quick assay method for asparagine  
 CC protease of plant origin. The asparagine protease specifically recognises  
 CC asparagine residues and cleaves proteins at the C-terminal end of the  
 CC asparagine residue. The assay uses a fluorescence substrate (which has  
 CC quenching properties) which distributes a 7-methoxy coumarin-4-yl-acetyl  
 CC group to the amino group of the glycine residue at the N-terminal side,  
 CC and a 2,4-dinitrophenyl group to the C-terminal of an amino acid  
 CC sequence. The fluorescence caused by the fluorescence substrate is not  
 CC connected to the asparagine residue and can be measured after cleavage by  
 CC the protease. The method is useful for assaying asparagine proteases of  
 CC plant origin. The activity of the protease can be determined within a  
 CC short time period and the enzyme activity can be measured with high  
 CC sensitivity using the fluorescence substrate. The procedure is quick even  
 CC when materials which inhibit other protease and fluorescence are included  
 CC in the sample  
 XX  
 SQ Sequence 11 AA;

Query Match 27.3%; Score 3; DB 3; Length 11;  
 Best Local Similarity 100.0%; Pred. No. 7.9e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 KSR 5  
 |||  
 Db 2 KSR 4

RESULT 52  
 AAY81924  
 ID AAY81924 standard; peptide; 11 AA.  
 XX  
 AC AAY81924;  
 XX  
 DT 23-JUN-2000 (first entry)



XX  
 DE Asparagine protease recognition peptide.  
 XX  
 KW Asparagine protease recognition peptide; protease assay; enzyme cleavage;  
 KW plant protease.  
 XX  
 OS Glycine max.  
 XX  
 PN JP3015886-B1.  
 XX  
 PD 06-MAR-2000.  
 XX  
 PF 04-NOV-1998; 98JP-00327536.  
 XX  
 PR 04-NOV-1998; 98JP-00327536.  
 XX  
 PA (NORQ ) NORINSUISANSHO SHOKUHIN SOGO.  
 XX  
 DR WPI; 2000-342275/30.  
 XX  
 PT Quick assay method of specific end protease activity of asparagine  
 PT residue of plant origin, involves distributing 7-methoxy phosphorous 4-yl  
 PT -acetyl and 2,4-dinitrophenyl group to N-terminal side and C-terminal  
 PT side.  
 XX  
 PS Example 2; Page 9; 11pp; Japanese.  
 XX  
 CC This sequence represents a peptide recognised and cleaved by asparagine  
 CC protease. The invention relates to a quick assay method for asparagine  
 CC protease of plant origin. The asparagine protease specifically recognises  
 CC asparagine residues and cleaves proteins at the C-terminal end of the  
 CC asparagine residue. The assay uses a fluorescence substrate (which has  
 CC quenching properties) which distributes a 7-methoxy coumarin-4-yl-acetyl  
 CC group to the amino group of the glycine residue at the N-terminal side,  
 CC and a 2,4-dinitrophenyl group to the C-terminal of an amino acid  
 CC sequence. The fluorescence caused by the fluorescence substrate is not  
 CC connected to the asparagine residue and can be measured after cleavage by  
 CC the protease. The method is useful for assaying asparagine proteases of  
 CC plant origin. The activity of the protease can be determined within a  
 CC short time period and the enzyme activity can be measured with high  
 CC sensitivity using the fluorescence substrate. The procedure is quick even  
 CC when materials which inhibit other protease and fluorescence are included  
 CC in the sample  
 XX  
 SQ Sequence 11 AA;

Query Match 27.3%; Score 3; DB 3; Length 11;  
 Best Local Similarity 100.0%; Pred. No. 7.9e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 KSR 5  
 |||  
 Db 2 KSR 4

RESULT 53  
 AAY81916

ID AAY81916 standard; peptide; 11 AA.  
 XX  
 AC AAY81916;  
 XX  
 DT 23-JUN-2000 (first entry)  
 XX  
 DE Asparagine protease recognition peptide.  
 XX  
 KW Asparagine protease recognition peptide; protease assay; enzyme cleavage;  
 KW plant protease.  
 XX  
 OS Glycine max.  
 XX  
 PN JP3015886-B1.  
 XX  
 PD 06-MAR-2000.  
 XX  
 PF 04-NOV-1998; 98JP-00327536.  
 XX  
 PR 04-NOV-1998; 98JP-00327536.  
 XX  
 PA (NORQ ) NORINSUISANSHO SHOKUHIN SOGO.  
 XX  
 DR WPI; 2000-342275/30.  
 XX  
 PT Quick assay method of specific end protease activity of asparagine  
 PT residue of plant origin, involves distributing 7-methoxy phosphorous 4-yl  
 PT -acetyl and 2,4-dinitrophenyl group to N-terminal side and C-terminal  
 PT side.  
 XX  
 PS Claim 1; Page 8; 11pp; Japanese.  
 XX  
 CC This sequence represents a peptide recognised and cleaved by asparagine  
 CC protease. The invention relates to a quick assay method for asparagine  
 CC protease of plant origin. The asparagine protease specifically recognises  
 CC asparagine residues and cleaves proteins at the C-terminal end of the  
 CC asparagine residue. The assay uses a fluorescence substrate (which has  
 CC quenching properties) which distributes a 7-methoxy coumarin-4-yl-acetyl  
 CC group to the amino group of the glycine residue at the N-terminal side,  
 CC and a 2,4-dinitrophenyl group to the C-terminal of an amino acid  
 CC sequence. The fluorescence caused by the fluorescence substrate is not  
 CC connected to the asparagine residue and can be measured after cleavage by  
 CC the protease. The method is useful for assaying asparagine proteases of  
 CC plant origin. The activity of the protease can be determined within a  
 CC short time period and the enzyme activity can be measured with high  
 CC sensitivity using the fluorescence substrate. The procedure is quick even  
 CC when materials which inhibit other protease and fluorescence are included  
 CC in the sample  
 XX  
 SQ Sequence 11 AA;

Query Match 27.3%; Score 3; DB 3; Length 11;  
 Best Local Similarity 100.0%; Pred. No. 7.9e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 KSR 5  
 |||

## RESULT 54

AAY81919

ID AAY81919 standard; peptide; 11 AA.

XX

AC AAY81919;

XX

DT 23-JUN-2000 (first entry)

XX

DE Asparagine protease recognition peptide.

XX

KW Asparagine protease recognition peptide; protease assay; enzyme cleavage;  
KW plant protease.

XX

OS Glycine max.

XX

PN JP3015886-B1.

XX

PD 06-MAR-2000.

XX

PF 04-NOV-1998; 98JP-00327536.

XX

PR 04-NOV-1998; 98JP-00327536.

XX

PA (NORQ ) NORINSUISANSHO SHOKUHIN SOGO.

XX

DR WPI; 2000-342275/30.

XX

PT Quick assay method of specific end protease activity of asparagine  
PT residue of plant origin, involves distributing 7-methoxy phosphorous 4-yl  
PT -acetyl and 2,4-dinitrophenyl group to N-terminal side and C-terminal  
PT side.

XX

PS Claim 1; Page 9; 11pp; Japanese.

XX

CC This sequence represents a peptide recognised and cleaved by asparagine  
CC protease. The invention relates to a quick assay method for asparagine  
CC protease of plant origin. The asparagine protease specifically recognises  
CC asparagine residues and cleaves proteins at the C-terminal end of the  
CC asparagine residue. The assay uses a fluorescence substrate (which has  
CC quenching properties) which distributes a 7-methoxy coumarin-4-yl-acetyl  
CC group to the amino group of the glycine residue at the N-terminal side,  
CC and a 2,4-dinitrophenyl group to the C-terminal of an amino acid  
CC sequence. The fluorescence caused by the fluorescence substrate is not  
CC connected to the asparagine residue and can be measured after cleavage by  
CC the protease. The method is useful for assaying asparagine proteases of  
CC plant origin. The activity of the protease can be determined within a  
CC short time period and the enzyme activity can be measured with high  
CC sensitivity using the fluorescence substrate. The procedure is quick even  
CC when materials which inhibit other protease and fluorescence are included  
CC in the sample

XX

SQ Sequence 11 AA;

Query Match

27.3%; Score 3; DB 3; Length 11;

Best Local Similarity 100.0%; Pred. No. 7.9e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 KSR 5  
|||  
Db 2 KSR 4

RESULT 55

AAY81918

ID AAY81918 standard; peptide; 11 AA.

XX

AC AAY81918;

XX

DT 23-JUN-2000 (first entry)

XX

DE Asparagine protease recognition peptide.

XX

KW Asparagine protease recognition peptide; protease assay; enzyme cleavage;  
KW plant protease.

XX

OS Glycine max.

XX

PN JP3015886-B1.

XX

PD 06-MAR-2000.

XX

PF 04-NOV-1998; 98JP-00327536.

XX

PR 04-NOV-1998; 98JP-00327536.

XX

PA (NORQ ) NORINSUISANSHO SHOKUHIN SOGO.

XX

DR WPI; 2000-342275/30.

XX

PT Quick assay method of specific end protease activity of asparagine  
PT residue of plant origin, involves distributing 7-methoxy phosphorous 4-yl  
PT -acetyl and 2,4-dinitrophenyl group to N-terminal side and C-terminal  
PT side.

XX

PS Claim 1; Page 9; 11pp; Japanese.

XX

CC This sequence represents a peptide recognised and cleaved by asparagine  
CC protease. The invention relates to a quick assay method for asparagine  
CC protease of plant origin. The asparagine protease specifically recognises  
CC asparagine residues and cleaves proteins at the C-terminal end of the  
CC asparagine residue. The assay uses a fluorescence substrate (which has  
CC quenching properties) which distributes a 7-methoxy coumarin-4-yl-acetyl  
CC group to the amino group of the glycine residue at the N-terminal side,  
CC and a 2,4-dinitrophenyl group to the C-terminal of an amino acid  
CC sequence. The fluorescence caused by the fluorescence substrate is not  
CC connected to the asparagine residue and can be measured after cleavage by  
CC the protease. The method is useful for assaying asparagine proteases of  
CC plant origin. The activity of the protease can be determined within a  
CC short time period and the enzyme activity can be measured with high  
CC sensitivity using the fluorescence substrate. The procedure is quick even  
CC when materials which inhibit other protease and fluorescence are included

CC in the sample  
XX  
SQ Sequence 11 AA;

Query Match 27.3%; Score 3; DB 3; Length 11;  
Best Local Similarity 100.0%; Pred. No. 7.9e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 KSR 5  
|||  
Db 2 KSR 4

RESULT 56

AAY81920

ID AAY81920 standard; peptide; 11 AA.

XX

AC AAY81920;

XX

DT 23-JUN-2000 (first entry)

XX

DE Asparagine protease recognition peptide.

XX

KW Asparagine protease recognition peptide; protease assay; enzyme cleavage;  
KW plant protease.

XX

OS Glycine max.

XX

PN JP3015886-B1.

XX

PD 06-MAR-2000.

XX

PF 04-NOV-1998; 98JP-00327536.

XX

PR 04-NOV-1998; 98JP-00327536.

XX

PA (NORQ ) NORINSUISANSHO SHOKUHHIN SOGO.

XX

DR WPI; 2000-342275/30.

XX

PT Quick assay method of specific end protease activity of asparagine  
PT residue of plant origin, involves distributing 7-methoxy phosphorous 4-yl  
PT -acetyl and 2,4-dinitrophenyl group to N-terminal side and C-terminal  
PT side.

XX

PS Claim 1; Page 9; 11pp; Japanese.

XX

CC This sequence represents a peptide recognised and cleaved by asparagine  
CC protease. The invention relates to a quick assay method for asparagine  
CC protease of plant origin. The asparagine protease specifically recognises  
CC asparagine residues and cleaves proteins at the C-terminal end of the  
CC asparagine residue. The assay uses a fluorescence substrate (which has  
CC quenching properties) which distributes a 7-methoxy coumarin-4-yl-acetyl  
CC group to the amino group of the glycine residue at the N-terminal side,  
CC and a 2,4-dinitrophenyl group to the C-terminal of an amino acid  
CC sequence. The fluorescence caused by the fluorescence substrate is not  
CC connected to the asparagine residue and can be measured after cleavage by

CC the protease. The method is useful for assaying asparagine proteases of  
CC plant origin. The activity of the protease can be determined within a  
CC short time period and the enzyme activity can be measured with high  
CC sensitivity using the fluorescence substrate. The procedure is quick even  
CC when materials which inhibit other protease and fluorescence are included  
CC in the sample

XX

SQ Sequence 11 AA;

Query Match 27.3%; Score 3; DB 3; Length 11;  
Best Local Similarity 100.0%; Pred. No. 7.9e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 KSR 5

|||

Db 2 KSR 4

#### RESULT 57

AAAY81917

ID AAAY81917 standard; peptide; 11 AA.

XX

AC AAAY81917;

XX

DT 23-JUN-2000 (first entry)

XX

DE Asparagine protease recognition peptide.

XX

KW Asparagine protease recognition peptide; protease assay; enzyme cleavage;  
KW plant protease.

XX

OS Glycine max.

XX

PN JP3015886-B1.

XX

PD 06-MAR-2000.

XX

PF 04-NOV-1998; 98JP-00327536.

XX

PR 04-NOV-1998; 98JP-00327536.

XX

PA (NORQ ) NORINSUISANSHO SHOKUHHIN SOGO.

XX

DR WPI; 2000-342275/30.

XX

PT Quick assay method of specific end protease activity of asparagine  
PT residue of plant origin, involves distributing 7-methoxy phosphorous 4-yl  
PT -acetyl and 2,4-dinitrophenyl group to N-terminal side and C-terminal  
PT side.

XX

PS Claim 1; Page 8; 11pp; Japanese.

XX

CC This sequence represents a peptide recognised and cleaved by asparagine  
CC protease. The invention relates to a quick assay method for asparagine  
CC protease of plant origin. The asparagine protease specifically recognises  
CC asparagine residues and cleaves proteins at the C-terminal end of the  
CC asparagine residue. The assay uses a fluorescence substrate (which has

CC quenching properties) which distributes a 7-methoxy coumarin-4-yl-acetyl  
CC group to the amino group of the glycine residue at the N-terminal side,  
CC and a 2,4-dinitrophenyl group to the C-terminal of an amino acid  
CC sequence. The fluorescence caused by the fluorescence substrate is not  
CC connected to the asparagine residue and can be measured after cleavage by  
CC the protease. The method is useful for assaying asparagine proteases of  
CC plant origin. The activity of the protease can be determined within a  
CC short time period and the enzyme activity can be measured with high  
CC sensitivity using the fluorescence substrate. The procedure is quick even  
CC when materials which inhibit other protease and fluorescence are included  
CC in the sample  
XX  
SQ Sequence 11 AA;

Query Match 27.3%; Score 3; DB 3; Length 11;  
Best Local Similarity 100.0%; Pred. No. 7.9e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 KSR 5  
|||  
Db 2 KSR 4

RESULT 58

AAY81921

ID AAY81921 standard; peptide; 11 AA.

XX

AC AAY81921;

XX

DT 23-JUN-2000 (first entry)

XX

DE Asparagine protease recognition peptide.

XX

KW Asparagine protease recognition peptide; protease assay; enzyme cleavage;  
KW plant protease.

XX

OS Glycine max.

XX

PN JP3015886-B1.

XX

PD 06-MAR-2000.

XX

PF 04-NOV-1998; 98JP-00327536.

XX

PR 04-NOV-1998; 98JP-00327536.

XX

PA (NORQ ) NORINSUISANSHO SHOKUHIN SOGO.

XX

DR WPI; 2000-342275/30.

XX

PT Quick assay method of specific end protease activity of asparagine  
PT residue of plant origin, involves distributing 7-methoxy phosphorous 4-yl  
PT -acetyl and 2,4-dinitrophenyl group to N-terminal side and C-terminal  
PT side.

XX

PS Example 2; Page 9; 11pp; Japanese.

XX

CC This sequence represents a peptide recognised and cleaved by asparagine  
CC protease. The invention relates to a quick assay method for asparagine  
CC protease of plant origin. The asparagine protease specifically recognises  
CC asparagine residues and cleaves proteins at the C-terminal end of the  
CC asparagine residue. The assay uses a fluorescence substrate (which has  
CC quenching properties) which distributes a 7-methoxy coumarin-4-yl-acetyl  
CC group to the amino group of the glycine residue at the N-terminal side,  
CC and a 2,4-dinitrophenyl group to the C-terminal of an amino acid  
CC sequence. The fluorescence caused by the fluorescence substrate is not  
CC connected to the asparagine residue and can be measured after cleavage by  
CC the protease. The method is useful for assaying asparagine proteases of  
CC plant origin. The activity of the protease can be determined within a  
CC short time period and the enzyme activity can be measured with high  
CC sensitivity using the fluorescence substrate. The procedure is quick even  
CC when materials which inhibit other protease and fluorescence are included  
CC in the sample  
XX  
SQ Sequence 11 AA;

Query Match 27.3%; Score 3; DB 3; Length 11;  
Best Local Similarity 100.0%; Pred. No. 7.9e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 KSR 5  
|||  
Db 2 KSR 4

RESULT 59

AAB16453

ID AAB16453 standard; peptide; 11 AA.

XX

AC AAB16453;

XX

DT 27-OCT-2000 (first entry)

XX

DE Linear peptide that binds to angiostatin SEQ ID # 4.

XX

KW Angiogenesis-inhibiting protein receptor; angiogenesis; angiostatin;  
KW endostatin; plasminogen; laminin; treatment; wound healing; solid tumour;  
KW psoriasis; scleroderma; myocardial angiogenesis; Crohn's disease;  
KW cerebral collateral; arteriovenous malformation; rubeosis; cancer;  
KW diabetic retinopathy; arthritis; wound healing; peptic ulcer;  
KW Helicobacter related disease; fracture; cat scratch fever.

XX

OS Synthetic.

XX

PN WO200032631-A2.

XX

PD 08-JUN-2000.

XX

PF 06-DEC-1999; 99WO-US028897.

XX

PR 04-DEC-1998; 98US-00206059.

XX

PA (ENTR-) ENTREMED INC.

XX



PI Macdonald NJ, Sim KL;  
 XX  
 DR WPI; 2000-412290/35.  
 XX  
 PT New angiogenesis-inhibiting protein receptors, useful in methods for  
 PT treating diseases and processes that are mediated by angiogenesis, such  
 PT as solid tumors, psoriasis, scleroderma and myocardial angiogenesis.  
 XX  
 PS Claim 1; Page 35; 100pp; English.  
 XX  
 CC This invention relates to angiogenesis-inhibiting protein receptors, and  
 CC the DNA sequences encoding them. Angiogenesis is the generation of new  
 CC blood vessels into a tissue, and normally occurs in wound healing, foetal  
 CC and embryonal development and the formation of the corpus luteum,  
 CC endometrium and placenta. Angiostatin is a protein (see AAB16450 and  
 CC AAA68202) involved in angiogenesis, and has an amino acid sequence  
 CC similar to that of a plasminogen fragment (see murine plasminogen  
 CC AAB16490). Angiostatin has the ability to inhibit angiogenesis.  
 CC Endostatin is also an angiogenesis inhibiting protein (see AAB16451 and  
 CC AAA68203). Sequences AAA68242 and AAB16522 represent coding and protein  
 CC sequences of human laminin. Laminin is an angiostatin binding protein,  
 CC and some of the peptides of the invention share homology with regions of  
 CC laminin. Peptides AAB16452-B16521 (excluding AAB16490) are the  
 CC angiogenesis-inhibiting protein receptor fragments of the invention. The  
 CC peptides bind either angiostatin or endostatin and can be used in methods  
 CC for treating diseases and processes that are mediated by angiogenesis,  
 CC such as solid tumours, psoriasis, scleroderma, myocardial angiogenesis,  
 CC Crohn's disease, cerebral collaterals, arteriovenous malformations,  
 CC rubeosis, diabetic retinopathy, arthritis, wound healing, peptic ulcers,  
 CC Helicobacter related diseases, fractures, placentation and cat scratch  
 CC fever. They are useful for the detection and prognosis of cancer. DNA  
 CC sequences A628204-A628241 encode the peptides of the invention  
 XX  
 SQ Sequence 11 AA;

Query Match 27.3%; Score 3; DB 3; Length 11;  
 Best Local Similarity 100.0%; Pred. No. 7.9e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 AIK 11  
 |||  
 Db 5 AIK 7

# RESULT 60

AAAY88542

ID AAY88542 standard; peptide; 11 AA.

XX

AC AAY88542;

XX

DT 07-AUG-2000 (first entry)

XX

DE NCAM Ig1 binding peptide #14.

XX

KW NCAM; neural cell adhesion molecule; Ig1; immunoglobulin domain 1;

KW neurite outgrowth promoter; proliferation; nerve damage; sclerosis;

KW impaired myelination; stroke; Parkinson's disease; memory; schizophrenia;

KW Alzheimer's disease; diabetes mellitus; circadian clock; nephrosis;  
 KW treatment; prosthetic nerve guide; treatment; nervous system.  
 XX  
 OS Synthetic.  
 XX  
 PN WO200018801-A2.  
 XX  
 PD 06-APR-2000.  
 XX  
 PF 23-SEP-1999; 99WO-DK000500.  
 XX  
 PR 29-SEP-1998; 98DK-00001232.  
 PR 29-APR-1999; 99DK-00000592.  
 XX  
 PA (RONN/) RONN L C B.  
 PA (BOCK/) BOCK E.  
 PA (HOLM/) HOLM A.  
 PA (OLSE/) OLSEN M.  
 PA (OSTE/) OSTERGAARD S.  
 PA (JENS/) JENSEN P H.  
 PA (POUL/) POULSEN F M.  
 PA (SORO/) SOROKA V.  
 PA (RALE/) RALETS I.  
 PA (BERE/) BEREZIN V.  
 XX  
 PI Ronn LCB, Bock E, Holm A, Olsen M, Ostergaard S, Jensen PH;  
 PI Poulsen FM, Soroka V, Ralets I, Berezin V;  
 XX  
 DR WPI; 2000-293111/25.  
 XX  
 PT Compositions that bind neural cell adhesion molecules useful for treating  
 PT disorders of the nervous system and muscles e.g. Alzheimer's and  
 PT Parkinson's diseases.  
 XX  
 PS Example 4; Page 25; 119pp; English.  
 XX  
 CC Neural cell adhesion molecule (NCAM) is a cellular adhesion molecule.  
 CC NCAM is found in three forms, two of which are transmembrane forms, while  
 CC the third is attached via a lipid anchor to the cell membrane. All three  
 CC NCAM forms have an extracellular structure consisting five immunoglobulin  
 CC domains (Ig domains). The Ig domains are numbered 1 to 5 from the N-  
 CC terminal. The present sequence represents a peptide which binds to the  
 CC NCAM Ig1 domain. The peptide can be used in a compound which binds to  
 CC NCAM-Ig1/Ig2 domains, and is capable of stimulating or promoting neurite  
 CC outgrowth from NCAM presenting cells, and is also capable of promoting  
 CC the proliferation of NCAM presenting cells. The compound may be used in  
 CC the treatment of normal, degenerated or damaged NCAM presenting cells.  
 CC The compound may in particular be used to treat diseases of the central  
 CC and peripheral nervous systems such as post operative nerve damage,  
 CC traumatic nerve damage, impaired myelination of nerve fibres, conditions  
 CC resulting from a stroke, Parkinson's disease, Alzheimer's disease,  
 CC dementias, sclerosis, nerve degeneration associated with diabetes  
 CC mellitus, disorders affecting the circadian clock or neuro-muscular  
 CC transmission and schizophrenia. Conditions affecting the muscles may also  
 CC be treated with the compound, such as conditions associated with impaired  
 CC function of neuromuscular connections (e.g. genetic or traumatic shock or  
 CC traumatic atrophic muscle disorders). Conditions of the gonads, pancreas

CC (e.g. diabetes mellitus types I and II), kidney (e.g. nephrosis), heart,  
CC liver and bowel may also be treated using the compound. The compound is  
CC used in a prosthetic nerve guide, and also to stimulate the ability to  
CC learn, and to stimulate the memory of a subject  
XX  
SQ Sequence 11 AA;

Query Match 27.3%; Score 3; DB 3; Length 11;  
Best Local Similarity 100.0%; Pred. No. 7.9e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ARK 3  
|||  
Db 1 ARK 3

RESULT 61

AAAY88549

ID AAAY88549 standard; peptide; 11 AA.

XX

AC AAAY88549;

XX

DT 07-AUG-2000 (first entry)

XX

DE NCAM Igl binding peptide #21.

XX

KW NCAM; neural cell adhesion molecule; Igl; immunoglobulin domain 1;

KW neurite outgrowth promoter; proliferation; nerve damage; sclerosis;

KW impaired myelination; stroke; Parkinson's disease; memory; schizophrenia;

KW Alzheimer's disease; diabetes mellitus; circadian clock; nephrosis;

KW treatment; prosthetic nerve guide; treatment; nervous system.

XX

OS Synthetic.

XX

PN WO200018801-A2.

XX

PD 06-APR-2000.

XX

PF 23-SEP-1999; 99WO-DK000500.

XX

PR 29-SEP-1998; 98DK-00001232.

PR 29-APR-1999; 99DK-00000592.

XX

PA (RONN/) RONN L C B.

PA (BOCK/) BOCK E.

PA (HOLM/) HOLM A.

PA (OLSE/) OLSEN M.

PA (OSTE/) OSTERGAARD S.

PA (JENS/) JENSEN P H.

PA (POUL/) POULSEN F M.

PA (SORO/) SOROKA V.

PA (RALE/) RALETS I.

PA (BERE/) BEREZIN V.

XX

PI Ronn LCB, Bock E, Holm A, Olsen M, Ostergaard S, Jensen PH;

PI Poulsen FM, Soroka V, Ralets I, Berezin V;

XX

DR WPI; 2000-293111/25.  
 XX  
 PT Compositions that bind neural cell adhesion molecules useful for treating  
 PT disorders of the nervous system and muscles e.g. Alzheimer's and  
 PT Parkinson's diseases.  
 XX  
 PS Example 4; Page 25; 119pp; English.  
 XX  
 CC Neural cell adhesion molecule (NCAM) is a cellular adhesion molecule.  
 CC NCAM is found in three forms, two of which are transmembrane forms, while  
 CC the third is attached via a lipid anchor to the cell membrane. All three  
 CC NCAM forms have an extracellular structure consisting five immunoglobulin  
 CC domains (Ig domains). The Ig domains are numbered 1 to 5 from the N-  
 CC terminal. The present sequence represents a peptide which binds to the  
 CC NCAM Ig1 domain. The peptide can be used in a compound which binds to  
 CC NCAM-Ig1/Ig2 domains, and is capable of stimulating or promoting neurite  
 CC outgrowth from NCAM presenting cells, and is also capable of promoting  
 CC the proliferation of NCAM presenting cells. The compound may be used in  
 CC the treatment of normal, degenerated or damaged NCAM presenting cells.  
 CC The compound may in particular be used to treat diseases of the central  
 CC and peripheral nervous systems such as post operative nerve damage,  
 CC traumatic nerve damage, impaired myelination of nerve fibres, conditions  
 CC resulting from a stroke, Parkinson's disease, Alzheimer's disease,  
 CC dementias, sclerosis, nerve degeneration associated with diabetes  
 CC mellitus, disorders affecting the circadian clock or neuro-muscular  
 CC transmission and schizophrenia. Conditions affecting the muscles may also  
 CC be treated with the compound, such as conditions associated with impaired  
 CC function of neuromuscular connections (e.g. genetic or traumatic shock or  
 CC traumatic atrophic muscle disorders). Conditions of the gonads, pancreas  
 CC (e.g. diabetes mellitus types I and II), kidney (e.g. nephrosis), heart,  
 CC liver and bowel may also be treated using the compound. The compound is  
 CC used in a prosthetic nerve guide, and also to stimulate the ability to  
 CC learn, and to stimulate the memory of a subject  
 XX  
 SQ Sequence 11 AA;

Query Match 27.3%; Score 3; DB 3; Length 11;  
 Best Local Similarity 100.0%; Pred. No. 7.9e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 KSR 5  
 |||  
 Db 2 KSR 4

# RESULT 62

AAB10140

ID AAB10140 standard; peptide; 11 AA.

XX

AC AAB10140;

XX

DT 10-NOV-2000 (first entry)

XX

DE Insertion sequence ISS1/1 Polymerase N-terminal protein fragment 39/2.

XX

KW Insertion sequence; ISS1/1; heat stable polymerase;

KW 3'-5'-exonuclease activity.

XX  
 OS Unidentified.  
 XX  
 PN DE19859107-A1.  
 XX  
 PD 29-JUN-2000.  
 XX  
 PF 21-DEC-1998; 98DE-01059107.  
 XX  
 PR 21-DEC-1998; 98DE-01059107.  
 XX  
 PA (HOFF ) ROCHE DIAGNOSTICS GMBH.  
 XX  
 PI Frey B, Sobek H, Schmitz-Agheguian G, Thomm M, Kath-Petersen R;  
 XX  
 DR WPI; 2000-476975/42.  
 XX  
 PT New heat-stable polymerase from ISS1/1, useful for amplification of,  
 PT labeling and extending nucleic acids, has 3'-5'- but not 5'-3'-  
 PT exonuclease activity.  
 XX  
 PS Example 8; Page 11; 40pp; German.  
 XX  
 CC This invention describes a novel heat-stable polymerase (I), from ISS1/1  
 CC which is homologous to PolI of Escherichia coli, that has 3'-5'-  
 CC exonuclease activity but lacks 5'-3'-exonuclease activity. (I), and their  
 CC mutated/modified forms with reduced 3'-exonuclease activity, are used for  
 CC labeling, amplifying and extending nucleic acids, especially in  
 CC polymerase chain reactions, but also e.g. for nick translation and for  
 CC random-priming labeling reactions. Mutation of (I) allow its 3'-5'-  
 CC exonuclease activity, very strong in the native enzyme, to be adjusted to  
 CC suit particular applications, while retaining its high processivity  
 CC (which can be increased further when used with associated proteins). (I)  
 CC can generate very long (over 2 kb) amplicons, which requires only small  
 CC amounts of template sequences, and reduces accumulation of errors. This  
 CC sequence represents an N-terminal fragment of the insertion sequence  
 CC ISS1/1 polymerase described in the method of the invention  
 XX  
 SQ Sequence 11 AA;

Query Match 27.3%; Score 3; DB 3; Length 11;  
 Best Local Similarity 100.0%; Pred. No. 7.9e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 AIK 11  
 |||  
 Db 9 AIK 11

RESULT 63  
 AAY93544  
 ID AAY93544 standard; peptide; 11 AA.  
 XX  
 AC AAY93544;  
 XX  
 DT 25-SEP-2000 (first entry)  
 XX

DE Amino acid sequence of a synthetic protein transduction domain.  
 XX  
 KW Protein transduction system; protein transduction domain;  
 KW cytotoxic domain; pathogen infection; retroviral infection;  
 KW plasmodial infection; cancer; prostate cancer.  
 XX  
 OS Synthetic.  
 XX  
 PN WO200034308-A2.  
 XX  
 PD 15-JUN-2000.  
 XX  
 PF 10-DEC-1999; 99WO-US029289.  
 XX  
 PR 10-DEC-1998; 98US-0111701P.  
 XX  
 PA (UNIW ) UNIV WASHINGTON.  
 XX  
 PI Dowdy SF;  
 XX  
 DR WPI; 2000-431269/37.  
 XX  
 PT Protein transduction system for treating cancer and pathogenic infections  
 PT has a fusion protein comprising a protein transduction domain covalently  
 PT linked to a cytotoxic domain.  
 XX  
 PS Claim 66; Page 98; 127pp; English.  
 XX  
 CC AAY93542-51 represent synthetic protein transduction domains, which are  
 CC used in the protein transduction system of the invention. The  
 CC specification describes a protein transduction system, which comprises a  
 CC fusion protein. This fusion protein has a covalently linked protein  
 CC transduction domain and cytotoxic domain. The system is useful for  
 CC treating pathogen infection in mammals, infections such as those caused  
 CC by CMV, HSV-1, HCV, KSHV, yellow fever virus, flavivirus or rhinovirus,  
 CC retroviral infections such as HIV-1, HIV-2, HTVL-3 and/or LAV, plasmodial  
 CC infections associated with P.faciparum, P.vivax, P.ovale, P.malariae. It  
 CC is also useful for treating cancer, especially prostate cancer  
 XX  
 SQ Sequence 11 AA;

Query Match 27.3%; Score 3; DB 3; Length 11;  
 Best Local Similarity 100.0%; Pred. No. 7.9e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ARK 3  
 |||  
 Db 2 ARK 4

RESULT 64  
 AAB09423  
 ID AAB09423 standard; protein; 11 AA.  
 XX  
 AC AAB09423;  
 XX  
 DT 06-AUG-2003 (revised)

DT 30-AUG-2000 (first entry)  
 XX  
 DE Hepatitis GB virus protein sequence SEQ ID NO:550.  
 XX  
 KW Hepatitis GB virus; HGBV; diagnosis; therapeutic; immunogenic; infection;  
 KW detection; characterisation; hepatitis.  
 XX  
 OS Hepatitis GB virus.  
 XX  
 PN US6051374-A.  
 XX  
 PD 18-APR-2000.  
 XX  
 PF 07-JUN-1995; 95US-00488445.  
 XX  
 PR 14-FEB-1994; 94US-00196030.  
 PR 13-MAY-1994; 94US-00242654:  
 PR 29-JUL-1994; 94US-00283314.  
 PR 23-NOV-1994; 94US-00344185.  
 PR 23-NOV-1994; 94US-00344190.  
 PR 30-JAN-1995; 95US-00377557.  
 XX  
 PA (ABBO ) ABBOTT LAB.  
 XX  
 PI Dawson GJ, Leary TP, Muerhoff AS, Pilot-Matias TJ, Buijk SL;  
 PI Mushahwar IK, Simons JN, Desai SM, Erker JC, Schlauder GG;  
 XX  
 DR WPI; 2000-338307/29.  
 XX  
 PT Detecting target hepatitis GB virus nucleic acid in a test sample  
 PT suspected of containing HGBV comprises reacting the test sample the HGBV  
 PT polynucleotide probe and detecting the complex that contains target HGBV.  
 XX  
 PS Example 18; Col 549-550; 369pp; English.  
 XX  
 CC The present invention describe a method for detecting target hepatitis GB  
 CC virus (HGBV) nucleic acid (THN) in a test sample (T) suspected of  
 CC containing HGBV. The method involves reacting (T) with a HGBV  
 CC polynucleotide probe (I) containing 15 contiguous nucleotides, and which  
 CC selectively hybridises to the HGBV genome or its full complement, and  
 CC detecting the complex that contains THN, indicating the presence of  
 CC target HGBV. The method is used for detecting target HGBV nucleic acid in  
 CC the test sample suspected of containing HGBV and for characterisation of  
 CC newly ascertained etiological agent of non-A, non-B, non-C, non-D and non  
 CC -E hepatitis causing agents collectively termed as hepatitis GB virus.  
 CC AAA55270 to AAA55489 and AAB08985 to AAB09480 represent nucleotide and  
 CC protein sequences used in the exemplification of the present invention.  
 CC (Updated on 06-AUG-2003 to correct OS field.)  
 XX  
 SQ Sequence 11 AA;

Query Match 27.3%; Score 3; DB 3; Length 11;  
 Best Local Similarity 100.0%; Pred. No. 7.9e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 AIK 11  
 |||

## RESULT 65

AAY81393

ID AAY81393 standard; peptide; 11 AA.

XX

AC AAY81393;

XX

DT 19-JUN-2000 (first entry)

XX

DE PKC-alpha substrate peptide, used in detection of an SH-labelled oligo.

XX

KW Thermophilic rolling circle amplification; TRCA; circular template;

KW multimeric product; detection; single nucleotide polymorphism; SNP;

KW disulphide bond; PKC-alpha substrate; protein kinase C; fluorescent.

XX

OS Synthetic.

XX

PN WO200009738-A1.

XX

PD 24-FEB-2000.

XX

PF 17-AUG-1999; 99WO-US018808.

XX

PR 17-AUG-1998; 98US-0096830P.

PR 30-SEP-1998; 98US-00102535.

PR 03-NOV-1998; 98US-0106885P.

PR 03-NOV-1998; 98US-0106910P.

XX

PA (PACB ) PACKARD BIOSCIENCE CO.

XX

PI Woodward KL, Nallur GN, Taylor S;

XX

DR WPI; 2000-224363/19.

XX

PT Analyzing a sample polynucleotide for detecting single nucleotide

PT polymorphism by rolling circle amplification.

XX

PS Example 29; Page 105; 126pp; English.

XX

CC The invention relates to methods for sensitively detecting the presence  
CC of a particular nucleic acid in a sample, e.g., determining whether a  
CC sequence of interest contains a particular genetic event such as a single  
CC nucleotide polymorphism (SNP). The sample nucleotide to be analysed is  
CC contacted with a single-stranded circular template comprising at least  
CC one copy of a nucleotide sequence complementary to the sample sequence  
CC and a type 2S restriction enzyme recognition site containing one or more  
CC modified bases. The circular template is combined with nucleotide  
CC triphosphates, a polymerase and optionally, a TRCA (thermophilic rolling  
CC circle amplification) primer to yield a single stranded multimer  
CC complementary in sequence to the circular template. A cleavage probe is  
CC then added, which anneals to the type 2S restriction recognition sites in  
CC the multimer and circular template, creating double stranded restriction  
CC sites. On treatment with the appropriate enzyme, the multimer is cleaved  
CC at the restriction sites, while the circular template is less sensitive  
CC to cleavage, due to the presence of the modified base(s) in the



CC restriction site. The fragments produced can then be detected using an  
 CC array of capture probes immobilised on a matrix. The method is useful for  
 CC analysing nucleotide sequences in order to detect a genetic event such as  
 CC a SNP. The method is sensitive and specific for detecting the target  
 CC nucleotide sequence. The present sequence represents a fluorescent  
 CC donor/quencher-labelled protein kinase C (PKC) alpha substrate used in an  
 CC exemplification of the invention in the detection of thiol (SH)-labelled  
 CC oligonucleotides. The SH-labelled oligonucleotide is contacted with PKC-  
 CC alpha, and a disulphide bond is allowed to form between the  
 CC oligonucleotide and the PKC-alpha. The activity of the PKC-alpha is then  
 CC detected using this sequence  
 XX  
 SQ Sequence 11 AA;

Query Match 27.3%; Score 3; DB 3; Length 11;  
 Best Local Similarity 100.0%; Pred. No. 7.9e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ARK 3  
 |||  
 Db 1 ARK 3

# RESULT 66

AAY54479

ID AAY54479 standard; peptide; 11 AA.

XX

AC AAY54479;

XX

DT 25-APR-2000 (first entry)

XX

DE Peptide used to treat infections, inflammation and tumours.

XX

KW Polycationic peptide; infection; inflammation; tumour; lactoferrin;  
 KW lactoferricin; conalbumin; ovotransferrin; antimicrobial; synergist;  
 KW antibacterial; antiviral; antifungal; candidiasis; defensin; magainin;  
 KW cecropin; protegrin; indolicidin analogue; histone;  
 KW acquired immune deficiency syndrome.

XX

OS Unidentified.

XX

PN WO200000214-A2.

XX

PD 06-JAN-2000.

XX

PF 28-JUN-1999; 99WO-EP004067.

XX

PR 26-JUN-1998; 98NL-01009505.

PR 09-OCT-1998; 98NL-01010284.

PR 06-NOV-1998; 98EP-00203765.

XX

PA (NUTR-) NUTRICIA NV.

XX

PI Swart PJ, Kuipers ME, Meijer DKF, Hageman RJJ, Van Den Berg JJM;

XX

DR WPI; 2000-160640/14.

XX

PT Composition containing cationic protein or peptide and buffer, used to  
PT treat or prevent infections, inflammation and tumors, e.g. Candida.  
XX  
PS Claim 3; Page 43; 90pp; English.  
XX  
CC AAY54468-95 represent exemplary polycationic peptides which are used in  
CC medicaments for treating and preventing infections (by bacteria, fungi,  
CC viruses), inflammation and tumors. For peptides AAY54483-86, a peptide  
CC comprising one of these sequences is used. Polycationic peptides may be  
CC derived from human or bovine lactoferrin (preferred), lactoferricin, or  
CC conalbumin (ovotransferrin), as well as alpha or beta defensins,  
CC magainins, cecropins type A or B, protegrins, indolicidin analogues, and  
CC polycations isolatable from insects and histones. The medicament  
CC comprises a buffer which maintains a preselected pH in treated tissue.  
CC The buffer provides a tissue pH at which growth of Candida is reduced.  
CC The peptides show a synergistic effect when combined with known  
CC antimicrobials, so allow a reduction in the dose of such compounds. The  
CC medicaments are used to treat and/or prevent infections, inflammation and  
CC tumors, or when used with separately administered antibacterial,  
CC antiviral or antifungal agents, to provide a synergistic effect,  
CC especially for treating candidiasis, e.g. in patients with acquired  
CC immune deficiency syndrome  
XX  
SQ Sequence 11 AA;

Query Match 27.3%; Score 3; DB 3; Length 11;  
Best Local Similarity 100.0%; Pred. No. 7.9e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 KSR 5  
| | |  
Db 1 KSR 3

# RESULT 67

AAB29416

ID AAB29416 standard; peptide; 11 AA.

XX

AC AAB29416;

XX

DT 09-FEB-2001 (first entry)

XX

DE Synthetic transduction domain, SEQ ID NO:3.

XX

KW Protein transduction domain; fusion molecule; therapeutic agent;  
KW drug targetting; drug discovery; cell transduction; bioavailability;  
KW vaccine; nervous system disorder; Alzheimer's disease;  
KW Parkinson's disease; Huntington's disease; pre-senile dementia; epilepsy;  
KW seizure; compulsive behaviour; meningitis; encephalitis; ischaemia;  
KW spongiform encephalopathy; dyslexia; age-related memory loss;  
KW Lou Gehring's disease; viral infection; HIV; bacterial infection.

XX

OS Synthetic.

XX

PN WO200062067-A1.

XX

PD 19-OCT-2000.

XX  
 PF 28-FEB-2000; 2000WO-US005097.  
 XX  
 PR 28-FEB-1999; 99US-0122757P.  
 PR 29-AUG-1999; 99US-0151291P.  
 XX  
 PA (UNIW ) UNIV WASHINGTON.  
 XX  
 PI Dowdy SF;  
 XX  
 DR WPI; 2000-647439/62.  
 XX  
 PT Fusion molecules comprising protein transduction domains and therapeutic  
 PT agents, useful for treating e.g. Alzheimer's and Parkinson's diseases,  
 PT dementia and epilepsy.  
 XX  
 PS Claim 36; Page 147; 191pp; English.  
 XX  
 CC The invention relates to a novel fusion molecule comprising at least one  
 CC protein transduction domain (PTD) and at least one linked molecule, where  
 CC the linked molecule has therapeutic or prophylactic activity against a  
 CC medical condition. The invention also relates to methods of drug  
 CC discovery in which the test compound is linked to a suitable transducing  
 CC protein and introduced to a cell; a method of killing resistant  
 CC microorganisms using a suitable fusion molecule; a mammal comprising a  
 CC covalently linked fusion molecule; and a mammal adapted for experimental  
 CC use in which at least one transduction molecule has been transduced into  
 CC essentially all the cells of the mammal. The fusion molecule is used to  
 CC deliver a therapeutic agent to a mammal, especially a human. The linked  
 CC molecule may be a vaccine, an anti-infective drug, a cardiovascular drug,  
 CC an antitumour drug, an analgesic, an antiinflammatory, a diagnostic  
 CC marker or a drug for the treatment or prevention of a central or  
 CC peripheral nervous system disorder. The central nervous system (CNS)  
 CC disorder is especially Alzheimer's disease, Parkinson's disease,  
 CC Huntington's disease, and also includes pre-senile dementia, epilepsy and  
 CC seizures, compulsive behaviour, meningitis (including viral and bacterial  
 CC meningitis), encephalitis, ischaemia, scrapie (or related spongiform  
 CC encephalopathies), dyslexia, age-related memory loss or Lou Gehring's  
 CC disease. Fusion molecules can also be used to kill virally infected  
 CC cells, especially those infected with HIV. The vaccines are used to treat  
 CC or prevent bacterial or viral infections. The methods are a highly  
 CC effective means for transducing a molecule into an entire mammal or into  
 CC specific cells, tissues, organs and systems within it. They also overcome  
 CC bioavailability problems that are associated with many therapeutic agents  
 CC (e.g., large molecular size, hydrophobicity, hydrophilicity, biological  
 CC resistance), by providing efficient transduction of the target cell. The  
 CC present sequence represents a specifically claimed protein transduction  
 CC domain  
 XX  
 SQ Sequence 11 AA;

Query Match 27.3%; Score 3; DB 3; Length 11;  
 Best Local Similarity 100.0%; Pred. No. 7.9e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ARK 3  
 |||

## RESULT 68

AAB26504

ID AAB26504 standard; peptide; 11 AA.

XX

AC AAB26504;

XX

DT 11-JAN-2001 (first entry)

XX

DE Human IgE C epsilon4 domain epitope P8.

XX

KW IgE; C epsilon3; C epsilon4; histamine release inhibitor; vaccine;  
KW antibody; epitope; mimotope; human.

XX

OS Homo sapiens.

XX

PN WO200050461-A1.

XX

PD 31-AUG-2000.

XX

PF 22-FEB-2000; 2000WO-EP001456.

XX

PR 25-FEB-1999; 99GB-00004408.

PR 21-JUL-1999; 99GB-00017144.

PR 07-AUG-1999; 99GB-00018598.

PR 07-AUG-1999; 99GB-00018599.

PR 07-AUG-1999; 99GB-00018601.

PR 07-AUG-1999; 99GB-00018604.

PR 07-AUG-1999; 99GB-00018606.

PR 29-OCT-1999; 99GB-00025618.

XX

PA (SMIK ) SMITHKLINE BEECHAM BIOLOGICALS.

PA (PEPT-) PEPTIDE THERAPEUTICS LTD.

XX

PI Friede M, Mason S, Turnell WG, Van Mechelen MP;

PI Vinals Y De BassolsC;

XX

DR WPI; 2000-572074/53.

XX

PT Peptides comprising surface exposed epitopes or mimotopes derived from C-  
PT epsilon-3 or C-epsilon-4 domains of IgE, useful for preventing or  
PT treating allergy.

XX

PS 4; Page 4; 76pp; English.

XX

CC The present invention relates epitopes and mimotopes of an isolated  
CC surface exposed epitope of C epsilon3 or C epsilon4 domain of IgE. The  
CC epitopes were identified by calculating the accessible surface of each  
CC IgE residue. Mimotopes were designed to be similar to the epitopes. The  
CC epitopes are useful in preparing medicaments for treating or preventing  
CC allergies. The epitopes and mimotopes of the invention induce anti-IgE  
CC antibodies which are capable of raising non-anaphylactic antibodies and  
CC inhibiting histamine release. The present sequence is an IgE C epsilon4  
CC domain epitope

XX

SQ Sequence 11 AA;

Query Match 27.3%; Score 3; DB 3; Length 11;  
Best Local Similarity 100.0%; Pred. No. 7.9e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 SRD 6  
| | |  
Db 6 SRD 8

RESULT 69

AAB08569

ID AAB08569 standard; peptide; 11 AA.

XX

AC AAB08569;

XX

DT 20-DEC-2000 (first entry)

XX

DE Peptide identified from a databank of polypeptides and polynucleotides.

XX

KW Precursor peptide; polypeptide hormone; peptide identification.

XX

OS Unidentified.

XX

FH Key Location/Qualifiers

FT Modified-site 1

FT /note= "hydrogen attached"

FT Modified-site 11

FT /note= "amidated residue"

XX

PN WO200050636-A1.

XX

PD 31-AUG-2000.

XX

PF 24-FEB-2000; 2000WO-FR000460.

XX

PR 25-FEB-1999; 99US-00257525.

XX

PA (SCRC ) SCRAS SOC CONSEILS RECH & APPL SCI.

PA (CNRS ) CNRS CENT NAT RECH SCI.

XX

PI Camara Y FerrerJA, Thurieau C, Martinez J, Berge G, Goze C;

XX

DR WPI; 2000-572101/53.

XX

PT Identifying peptide with selected function, useful particularly for C-

PT amidated hormones, by screening database for combination of nucleic acid

PT and amino acid sequences. --

XX

PS Disclosure; Page 21; 40pp; French.

XX

CC The specification describes a method for identifying a peptide having a

CC particular function. The method comprises preparing a database of

CC polynucleotides and polypeptides of unknown functions, screening the

CC database for a combination of nucleotides or amino acids indicative of

CC the peptide with a particular function, and identifying polynucleotides

CC and proteins which contain the peptide. The method is used to identify  
CC precursor peptides with an amidated C-terminus, especially polypeptide  
CC hormones, for studying physiologically active substances. The present  
CC sequence represents a peptide which was identified using the method of  
CC the invention

XX

SQ Sequence 11 AA;

Query Match 27.3%; Score 3; DB 3; Length 11;  
Best Local Similarity 100.0%; Pred. No. 7.9e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 DMT 8

|||

Db 6 DMT 8

#### RESULT 70

AAB08606

ID AAB08606 standard; peptide; 11 AA.

XX

AC AAB08606;

XX

DT 20-DEC-2000 (first entry)

XX

DE Peptide identified from an origin of spliceosome associated protein 114.

XX

KW Precursor peptide; polypeptide hormone; peptide identification.

XX

OS Unidentified.

XX

FH Key Location/Qualifiers

FT Modified-site 1

FT /note= "hydrogen attached"

FT Modified-site 11

FT /note= "amidated residue"

XX

PN WO200050636-A1.

XX

PD 31-AUG-2000.

XX

PF 24-FEB-2000; 2000WO-FR000460.

XX

PR 25-FEB-1999; 99US-00257525.

XX

PA (SCRC ) SCRAS SOC CONSEILS RECH & APPL SCI.

PA (CNRS ) CNRS CENT NAT RECH SCI.

XX

PI Camara Y FerrerJA, Thurieau C, Martinez J, Berge G, Goze C;

XX

DR WPI; 2000-572101/53.

XX

PT Identifying peptide with selected function, useful particularly for C-  
PT amidated hormones, by screening database for combination of nucleic acid  
PT and amino acid sequences.

XX

PS Disclosure; Page 22; 40pp; French.

XX  
CC The specification describes a method for identifying a peptide having a  
CC particular function. The method comprises preparing a database of  
CC polynucleotides and polypeptides of unknown functions, screening the  
CC database for a combination of nucleotides or amino acids indicative of  
CC the peptide with a particular function, and identifying polynucleotides  
CC and proteins which contain the peptide. The method is used to identify  
CC precursor peptides with an amidated C-terminus, especially polypeptide  
CC hormones, for studying physiologically active substances. The present  
CC sequence represents a peptide which was identified using the method of  
CC the invention  
XX  
SQ Sequence 11 AA;

Query Match 27.3%; Score 3; DB 3; Length 11;  
Best Local Similarity 100.0%; Pred. No. 7.9e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 TAI 10  
| | |  
Db 9 TAI 11

RESULT 71

AAG65304

ID AAG65304 standard; protein; 11 AA.

XX

AC AAG65304;

XX

DT 30-NOV-2001 (first entry)

XX

DE Anti-IL-18 antibody 2E1 light chain CDR3 fragment.

XX

KW IL-18; interleukin-18; human; antibody; antirheumatic; cerebroprotective;  
KW nootropic; neurological; antiinflammatory; antiparkinsonian; cardiant;  
KW immunosuppressive; antidepressant; neuroleptic; hepatotropic; 2E1.

XX

OS Homo sapiens.

XX

PN WO200158956-A2.

XX

PD 16-AUG-2001.

XX

PF 09-FEB-2001; 2001WO-US004170.

XX

PR 10-FEB-2000; 2000US-0181608P.

XX

PA (BADI ) BASF AG.

XX

PI Ghayur T, Dixon RW, Roguska M, White M, Labkovsky B, Salfeld J;  
PI Duncan AR, Brocklehurst SM, Mankovich J, Shorrock CP, Thompson JE;  
PI Lennard SN;

XX

DR WPI; 2001-550020/61.

XX

PT Novel antibodies and compounds capable of binding to human interleukin-18  
PT useful for treating, e.g., inflammatory disorders, neurological

PT disorders, heart failure, myocardial infarction, and autoimmune diseases.  
XX  
PS Claim 27; Page 38; 91pp; English.  
XX  
CC The invention provides isolated antibodies, or antigen-binding portions,  
CC that are capable of binding to human interleukin-18 (IL-18). The  
CC antibodies may be used to inhibit human IL-18 activity in, and treat a  
CC disorder where IL-18 is detrimental in, a human subject suffering from,  
CC inflammatory disorders (e.g., rheumatoid arthritis, Crohn's disease,  
CC inflammatory bowel disease, and osteoarthritis), neurological disorders  
CC (e.g., Huntington's chorea, Parkinson's disease, Alzheimer's disease, and  
CC stroke), heart failure, myocardial infarction, autoimmune diseases such  
CC as autoimmune hepatitis and autoimmune neutropaenia, and mental disorders  
CC (e.g., depression and schizophrenia). Treatment with an anti-IL-18  
CC antibody may occur before, concurrent, or after administration of a  
CC second agent selected from an antibody, or fragment, capable of binding  
CC human IL-12, methotrexate, anti-tumor necrosis factor, corticosteroids,  
CC cyclosporin, rapamycin, FK506, and non-steroidal anti-inflammatory  
CC agents. The present sequence represents an anti-IL-18 antibody 2E1 light  
CC chain CDR3 fragment  
XX  
SQ Sequence 11 AA;

Query Match 27.3%; Score 3; DB 4; Length 11;  
Best Local Similarity 100.0%; Pred. No. 7.9e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 SRD 6  
    | | |  
Db 2 SRD 4

#### RESULT 72

AAB55201

ID AAB55201 standard; peptide; 11 AA.

XX

AC AAB55201;

XX

DT 05-MAR-2001 (first entry)

XX

DE Anti-RSV F1 DP178 region amino truncation peptide #8.

XX

KW Long lasting fusion peptide inhibitor; viral infection; antiviral;  
KW antifusogenic; mobile blood component; measles virus; MeV; SIV;  
KW simian immunodeficiency virus; human parainfluenza virus; HPIV; RSV;  
KW human respiratory syncytial virus; human immunodeficiency virus; HIV.

XX

OS Human respiratory syncytial virus.

XX

PN WO200069902-A1.

XX

PD 23-NOV-2000.

XX

PF 17-MAY-2000; 2000WO-US013651.

XX

PR 17-MAY-1999; 99US-0134406P.

PR 10-SEP-1999; 99US-0153406P.



XX  
PA (CONJ-) CONJUCHEM INC.  
XX  
PI Bridon DP, Dufresne RP, Boudjellab N, Robitaille M, Milner PG;  
XX  
DR WPI; 2001-007496/01.  
XX  
PT A modified peptide and a reactive group which is reactive with amino  
PT groups, hydroxyl groups, or thiol groups on blood components to form  
PT stable covalent bonds useful for treatment of viral infections, e.g.  
PT human immunodeficiency virus.  
XX  
PS Disclosure; Page 150; 211pp; English.  
XX  
CC The present invention describes a modified anti-viral peptide (I)  
CC comprising a peptide that exhibits anti-viral activity and a reactive  
CC group which is reactive with amino groups, hydroxyl groups, or thiol  
CC groups on blood components to form stable covalent bonds. (I) has anti-  
CC viral and anti-fusogenic activities. (I) inhibits viral infection of  
CC cells by inhibiting cell-cell fusion or free virus infection or to reduce  
CC the level of membrane fusion events between two or more entities, e.g.,  
CC virus-cell or cell-cell, relative to the level of membrane fusion that  
CC occurs in the absence of the peptide. (I) is useful in the treatment of  
CC patients who are suffering from viral infection, e.g. HIV, RSV, HPIV,  
CC MeV, and SIV. (I) may be administered prophylactically to previously  
CC uninfected individuals. This is useful in cases where an individual has  
CC been subjected to a high risk of exposure to a virus. By bonding of long-  
CC lived components of the blood, such as immunoglobulin, serum albumin, red  
CC blood cells and platelets the activity is extended for days to weeks.  
CC This is due to improved stability in vivo and a reduced susceptibility to  
CC peptidase or protease degradation. This minimises the need for more  
CC frequent, or even continual, administration of the peptides. AAB54784 to  
CC AAB55431 represent peptides used in the exemplification of the present  
CC invention  
XX  
SQ Sequence 11 AA;

Query Match 27.3%; Score 3; DB 4; Length 11;  
Best Local Similarity 100.0%; Pred. No. 7.9e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 RKS 4  
|||  
Db 5 RKS 7

# RESULT 73

AAE05275

ID AAE05275 standard; peptide; 11 AA.

XX

AC AAE05275;

XX

DT 12-SEP-2001 (first entry)

XX

DE Human immunodeficiency virus (HIV) TAT mutant peptide #2.

XX

KW DNA recombinase domain; protein transduction domain; PTD; mutant;

KW gene alteration; TAT protein; mutein; Human immunodeficiency virus; HIV.  
 XX  
 OS Human immunodeficiency virus.  
 OS Synthetic.  
 XX  
 PN WO200149832-A2.  
 XX  
 PD 12-JUL-2001.  
 XX  
 PF 05-JAN-2001; 2001WO-EP000060.  
 XX  
 PR 07-JAN-2000; 2000EP-00100351.  
 PR 10-NOV-2000; 2000EP-00124595.  
 XX  
 PA (ARTE-) ARTEMIS PHARM GMBH.  
 XX  
 PI Schwenk F;  
 XX  
 DR WPI; 2001-441873/47.  
 XX  
 PT Using site-specific DNA recombinase domain/protein transduction domain  
 PT fusion proteins for inducing target gene alterations in organisms or cell  
 PT cultures.  
 XX  
 PS Claim 5; Page 71; 85pp; English.  
 XX  
 CC The present invention relates to use of fusion proteins comprising a site  
 CC -specific DNA recombinase domain e.g. Cre and a protein transduction  
 CC domain (PTD) e.g. the Human immunodeficiency virus (HIV) derived TAT  
 CC peptide, for preparing an agent for inducing target gene alterations in a  
 CC living organism or cell culture. The present invention also provides a  
 CC method for inducing gene alterations in living organisms using the fusion  
 CC proteins of the invention. The present sequence is a HIV TAT mutant  
 CC peptide  
 XX  
 SQ Sequence 11 AA;

Query Match 27.3%; Score 3; DB 4; Length 11;  
 Best Local Similarity 100.0%; Pred. No. 7.9e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ARK 3  
 |||  
 Db 2 ARK 4

RESULT 74  
 AAG99815  
 ID AAG99815 standard; peptide; 11 AA.  
 XX  
 AC AAG99815;  
 XX  
 DT 27-SEP-2001 (first entry)  
 XX  
 DE ERA binding domain polypeptide SEQ ID NO 257.  
 XX  
 KW ERA binding domain; Escherichia coli; GTPase; antimicrobial;

KW antibacterial; antibiotic; pathogenesis; infection; vaccine;  
 KW peptide therapy.  
 XX  
 OS Schizosaccharomyces pombe.  
 XX  
 PN WO200153458-A2.  
 XX  
 PD 26-JUL-2001.  
 XX  
 PF 17-JAN-2001; 2001WO-US001786.  
 XX  
 PR 18-JAN-2000; 2000US-0176870P.  
 XX  
 PA (SMIK ) SMITHKLINE BEECHAM CORP.  
 PA (SMIK ) SMITHKLINE BEECHAM PLC.  
 XX  
 PI Lupas AN, Pearce KH;  
 XX  
 DR WPI; 2001-476108/51.  
 XX  
 PT New ERA binding domain polypeptides and polynucleotides encoding them,  
 PT useful as research reagents and materials for discovery of treatments and  
 PT diagnostics for diseases, or for genetic immunization.  
 XX  
 PS Claim 1; Page 36; 279pp; English.  
 XX  
 CC The present invention relates to ERA binding domain polypeptides  
 CC (AAG99559-AAG99989 and AAM00010-AAM00021). The era gene in Escherichia  
 CC coli codes for an essential GTPase protein able to autophosphorylate at  
 CC serine and/or threonine residues. The protein has potential antimicrobial  
 CC and antibacterial activity and is useful in screening for antagonists,  
 CC agonists and for compounds with antibiotic activity. The proteins are  
 CC also useful in determining their role in pathogenesis of infection,  
 CC dysfunction and disease and could be used as part of a vaccine and/or  
 CC peptide therapy  
 XX  
 SQ Sequence 11 AA;

Query Match 27.3%; Score 3; DB 4; Length 11;  
 Best Local Similarity 100.0%; Pred. No. 7.9e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ARK 3  
 |||  
 Db 7 ARK 9

# RESULT 75

ABB59308

ID ABB59308 standard; protein; 11 AA.

XX

AC ABB59308;

XX

DT 26-MAR-2002 (first entry)

XX

DE Drosophila melanogaster polypeptide SEQ ID NO 4716.

XX

KW Drosophila; developmental biology; cell signalling; insecticide;  
 KW pharmaceutical.  
 XX  
 OS Drosophila melanogaster.  
 XX  
 PN WO200171042-A2.  
 XX  
 PD 27-SEP-2001.  
 XX  
 PF 23-MAR-2001; 2001WO-US009231.  
 XX  
 PR 23-MAR-2000; 2000US-0191637P.  
 PR 11-JUL-2000; 2000US-00614150.  
 XX  
 PA (PEKE ) PE CORP NY.  
 XX  
 PI Venter JC, Adams M, Li PWD, Myers EW;  
 XX  
 DR WPI; 2001-656860/75.  
 DR N-PSDB; ABL03411.  
 XX  
 PT New isolated nucleic acid detection reagent for detecting 1000 or more  
 PT genes from Drosophila and for elucidating cell signaling and cell-cell  
 PT interactions.  
 XX  
 PS Disclosure; SEQ ID NO 4716; 21pp + Sequence Listing; English.  
 XX  
 CC The invention relates to an isolated nucleic acid detection reagent  
 CC capable of detecting 1000 or more genes from Drosophila. The invention is  
 CC useful in developmental biology and in elucidating cell signalling and  
 CC cell-cell interactions in higher eukaryotes for the development of  
 CC insecticides, therapeutics and pharmaceutical drugs. The invention  
 CC discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA  
 CC sequences (ABL01840-ABL16175) and the encoded proteins (ABB57737-  
 CC ABB72072). The sequence data for this patent did not form part of the  
 CC printed specification, but was obtained in electronic format directly  
 CC from WIPO at ftp.wipo.int/pub/published\_pct\_sequences  
 XX  
 SQ Sequence 11 AA;

Query Match 27.3%; Score 3; DB 4; Length 11;  
 Best Local Similarity 100.0%; Pred. No. 7.9e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 MTA 9  
 |||  
 Db 1 MTA 3

Search completed: April 8, 2004, 15:40:13  
 Job time : 44.3077 secs

OM protein - protein search, using sw model

Run on: April 8, 2004, 15:30:08 ; Search time 11.3077 Seconds  
(without alignments)  
50.221 Million cell updates/sec

Title: US-09-787-443A-22  
Perfect score: 11  
Sequence: 1 ARKSRDMTAIK 11

Scoring table: OLIGO  
Gapop 60.0 , Gapext 60.0

Searched: 389414 seqs, 51625971 residues

Word size : 0

Total number of hits satisfying chosen parameters: 8542

Minimum DB seq length: 11

Maximum DB seq length: 11

Post-processing: Listing first 100 summaries

Database : Issued\_Patents\_AA:\*  
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3: /cgn2\_6/ptodata/2/iaa/6A\_COMB.pep:\*  
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6: /cgn2\_6/ptodata/2/iaa/backfiles1.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	%		Query Match Length DB	ID	Description
	Score				
1	4	36.4	11	1	US-08-185-448-5 Sequence 5, Appli
2	4	36.4	11	2	US-08-747-137-63 Sequence 63, Appl
3	4	36.4	11	3	US-08-696-854B-3 Sequence 3, Appli
4	4	36.4	11	4	US-09-576-824A-547 Sequence 547, App
5	4	36.4	11	4	US-09-576-824A-548 Sequence 548, App
6	4	36.4	11	4	US-09-576-824A-549 Sequence 549, App
7	4	36.4	11	5	PCT-US91-08328-13 Sequence 13, Appl
8	3	27.3	11	1	US-07-851-941-12 Sequence 12, Appl
9	3	27.3	11	1	US-08-197-795-5 Sequence 5, Appli
10	3	27.3	11	1	US-08-431-539-10 Sequence 10, Appl
11	3	27.3	11	1	US-08-431-539-16 Sequence 16, Appl

12	3	27.3	11	1	US-08-615-181-84	Sequence 84, Appl
13	3	27.3	11	2	US-08-456-670B-28	Sequence 28, Appl
14	3	27.3	11	2	US-08-350-260A-340	Sequence 340, App
15	3	27.3	11	2	US-08-350-260A-342	Sequence 342, App
16	3	27.3	11	2	US-08-350-260A-349	Sequence 349, App
17	3	27.3	11	2	US-08-350-260A-375	Sequence 375, App
18	3	27.3	11	2	US-08-350-260A-424	Sequence 424, App
19	3	27.3	11	2	US-08-350-260A-427	Sequence 427, App
20	3	27.3	11	2	US-08-350-260A-430	Sequence 430, App
21	3	27.3	11	2	US-08-350-260A-516	Sequence 516, App
22	3	27.3	11	2	US-08-350-260A-522	Sequence 522, App
23	3	27.3	11	2	US-08-751-767A-29	Sequence 29, Appl
24	3	27.3	11	2	US-09-115-209-74	Sequence 74, Appl
25	3	27.3	11	3	US-08-817-926-6	Sequence 6, Appli
26	3	27.3	11	3	US-08-746-160-51	Sequence 51, Appl
27	3	27.3	11	3	US-08-810-324-46	Sequence 46, Appl
28	3	27.3	11	3	US-08-679-006-16	Sequence 16, Appl
29	3	27.3	11	3	US-09-183-217-9	Sequence 9, Appli
30	3	27.3	11	3	US-09-206-059-4	Sequence 4, Appli
31	3	27.3	11	3	US-09-208-966-3	Sequence 3, Appli
32	3	27.3	11	3	US-08-647-405B-3	Sequence 3, Appli
33	3	27.3	11	3	US-08-647-405B-4	Sequence 4, Appli
34	3	27.3	11	3	US-09-177-249-212	Sequence 212, App
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40	3	27.3	11	3	US-09-410-025-4	Sequence 4, Appli
41	3	27.3	11	3	US-09-410-025-5	Sequence 5, Appli
42	3	27.3	11	3	US-09-410-025-6	Sequence 6, Appli
43	3	27.3	11	3	US-09-410-025-7	Sequence 7, Appli
44	3	27.3	11	3	US-09-410-025-8	Sequence 8, Appli
45	3	27.3	11	3	US-09-410-025-9	Sequence 9, Appli
46	3	27.3	11	3	US-09-410-025-10	Sequence 10, Appl
47	3	27.3	11	4	US-09-025-769B-186	Sequence 186, App
48	3	27.3	11	4	US-09-227-357-567	Sequence 567, App
49	3	27.3	11	4	US-09-314-268-171	Sequence 171, App
50	3	27.3	11	4	US-09-277-599B-2	Sequence 2, Appli
51	3	27.3	11	4	US-09-149-476-698	Sequence 698, App
52	3	27.3	11	4	US-09-177-165A-1	Sequence 1, Appli
53	3	27.3	11	4	US-08-255-208A-77	Sequence 77, Appl
54	3	27.3	11	4	US-08-469-260A-550	Sequence 550, App
55	3	27.3	11	4	US-09-561-490E-56	Sequence 56, Appl
56	3	27.3	11	4	US-09-104-337A-340	Sequence 340, App
57	3	27.3	11	4	US-09-104-337A-342	Sequence 342, App
58	3	27.3	11	4	US-09-104-337A-349	Sequence 349, App
59	3	27.3	11	4	US-09-104-337A-375	Sequence 375, App
60	3	27.3	11	4	US-09-104-337A-424	Sequence 424, App
61	3	27.3	11	4	US-09-104-337A-427	Sequence 427, App
62	3	27.3	11	4	US-09-104-337A-430	Sequence 430, App
63	3	27.3	11	4	US-09-104-337A-516	Sequence 516, App
64	3	27.3	11	4	US-09-104-337A-522	Sequence 522, App
65	3	27.3	11	4	US-09-810-873-2	Sequence 2, Appli
66	3	27.3	11	4	US-08-488-446-550	Sequence 550, App
67	3	27.3	11	4	US-08-467-344A-550	Sequence 550, App
68	3	27.3	11	4	US-09-079-030-55	Sequence 55, Appl

69	3	27.3	11	4	US-09-591-694-38	Sequence 38, Appl
70	3	27.3	11	4	US-09-535-852-1119	Sequence 1119, Ap
71	3	27.3	11	4	US-09-535-852-1159	Sequence 1159, Ap
72	3	27.3	11	4	US-08-475-955-56	Sequence 56, Appl
73	3	27.3	11	4	US-09-775-052A-3	Sequence 3, Appli
74	3	27.3	11	4	US-09-576-824A-482	Sequence 482, App
75	3	27.3	11	4	US-09-576-824A-546	Sequence 546, App
76	3	27.3	11	5	PCT-US95-01721-5	Sequence 5, Appli
77	3	27.3	11	6	5187155-26	Patent No. 5187155
78	2	18.2	11	1	US-09-572-339-11	Sequence 11, Appl
79	2	18.2	11	1	US-07-596-081A-29	Sequence 29, Appl
80	2	18.2	11	1	US-07-696-551B-10	Sequence 10, Appl
81	2	18.2	11	1	US-07-666-719-20	Sequence 20, Appl
82	2	18.2	11	1	US-07-763-512-4	Sequence 4, Appli
83	2	18.2	11	1	US-07-719-692A-10	Sequence 10, Appl
84	2	18.2	11	1	US-07-621-670-7	Sequence 7, Appli
85	2	18.2	11	1	US-07-621-670-8	Sequence 8, Appli
86	2	18.2	11	1	US-07-924-753-13	Sequence 13, Appl
87	2	18.2	11	1	US-07-718-274A-10	Sequence 10, Appl
88	2	18.2	11	1	US-07-718-274A-23	Sequence 23, Appl
89	2	18.2	11	1	US-07-732-114A-7	Sequence 7, Appli
90	2	18.2	11	1	US-07-914-280-6	Sequence 6, Appli
91	2	18.2	11	1	US-07-807-022A-2	Sequence 2, Appli
92	2	18.2	11	1	US-07-838-264-3	Sequence 3, Appli
93	2	18.2	11	1	US-07-699-468-1	Sequence 1, Appli
94	2	18.2	11	1	US-07-699-468-2	Sequence 2, Appli
95	2	18.2	11	1	US-07-699-468-3	Sequence 3, Appli
96	2	18.2	11	1	US-07-699-468-7	Sequence 7, Appli
97	2	18.2	11	1	US-08-049-871-6	Sequence 6, Appli
98	2	18.2	11	1	US-08-049-871-8	Sequence 8, Appli
99	2	18.2	11	1	US-07-672-483-17	Sequence 17, Appl
100	2	18.2	11	1	US-07-791-935B-13	Sequence 13, Appl

#### ALIGNMENTS

##### RESULT 1

US-08-185-448-5

; Sequence 5, Application US/08185448

; Patent No. 5580747

##### ; GENERAL INFORMATION:

; APPLICANT: SHULTZ, JOHN W.

; APPLICANT: WHITE, DOUGLAS H.

; TITLE OF INVENTION: NON-RADIOACTIVE KINASE,

; TITLE OF INVENTION: PHOSPHATASE AND PROTEASE ASSAY

; NUMBER OF SEQUENCES: 11

##### ; CORRESPONDENCE ADDRESS:

; ADDRESSEE: ANDRUS, SCEALES, STARKE & SAWALL

; STREET: 100 E. WISCONSIN AVENUE, SUITE 1100

; CITY: MILWAUKEE

; STATE: WISCONSIN

; COUNTRY: USA

; ZIP: 53202

##### ; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

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;   OPERATING SYSTEM:  PC-DOS/MS-DOS
;   SOFTWARE:  PatentIn Release #1.0, Version
;   SOFTWARE:  #1.25
;   CURRENT APPLICATION DATA:
;   APPLICATION NUMBER:  US/08/185,448
;   FILING DATE:  21-JAN-1994
;   CLASSIFICATION:  435
;   PRIOR APPLICATION DATA:
;   APPLICATION NUMBER:  US 07/791,928
;   FILING DATE:  12-NOV-1991
;   ATTORNEY/AGENT INFORMATION:
;   NAME:  SARA, CHARLES S
;   REGISTRATION NUMBER:  30492
;   REFERENCE/DOCKET NUMBER:  F.3347-1
;   TELECOMMUNICATION INFORMATION:
;   TELEPHONE:  (608) 255-2022
;   TELEFAX:  (608) 255-2182
;   TELEX:  26832 ANDSTARK
;   INFORMATION FOR SEQ ID NO:  5:
;   SEQUENCE CHARACTERISTICS:
;   LENGTH:  11 amino acids
;   TYPE:  amino acid
;   TOPOLOGY:  linear
;   MOLECULE TYPE:  peptide
;   FEATURE:
;   NAME/KEY:  Binding-site
;   LOCATION:  1
;   OTHER INFORMATION:  /label= LABEL
;   OTHER INFORMATION:  /note= "LOCATION OF LISSAMINE RHODAMINE
;   OTHER INFORMATION:  DETECTION TAG"
US-08-185-448-5

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Query Match          36.4%;  Score 4;  DB 1;  Length 11;
Best Local Similarity 100.0%;  Pred. No. 1.4e+02;
Matches      4;  Conservative      0;  Mismatches      0;  Indels      0;  Gaps      0;

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Qy      2 RKSR 5
        ||||
Db      5 RKSR 8

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## RESULT 2

US-08-747-137-63

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; Sequence 63, Application US/08747137
; Patent No. 5945033
; GENERAL INFORMATION:
;   APPLICANT:  YEN, Richard C.K.
;   TITLE OF INVENTION:  NON-CROSSLINKED PROTEIN PARTICLES FOR
;   TITLE OF INVENTION:  THERAPEUTIC AND DIAGNOSTIC USE
;   NUMBER OF SEQUENCES:  184
;   CORRESPONDENCE ADDRESS:
;   ADDRESSEE:  Townsend and Townsend and Crew LLP
;   STREET:  Two Embarcadero Center, 8th Floor
;   CITY:  San Francisco
;   STATE:  CA
;   COUNTRY:  USA
;   ZIP:  94111

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; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/747,137
; FILING DATE: 12-NOV-1996
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/212,546
; FILING DATE: 14-MAR-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/069,831
; FILING DATE: 01-JUN-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/959,560
; FILING DATE: 13-OCT-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/641,720
; FILING DATE: 15-JAN-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Apple, Randolph T.
; REGISTRATION NUMBER: 36,429
; REFERENCE/DOCKET NUMBER: 016197-000840US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-576-0200
; INFORMATION FOR SEQ ID NO: 63:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: not relevant
US-08-747-137-63

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Query Match          36.4%; Score 4; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches      4; Conservative      0; Mismatches      0; Indels      0; Gaps      0;

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Qy      2 RKSR 5
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Db      5 RKSR 8

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# RESULT 3

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US-08-696-854B-3
; Sequence 3, Application US/08696854B
; Patent No. 6017878
; GENERAL INFORMATION:
; APPLICANT: SARAGOVI, Uri H.
; APPLICANT: LeSAUTEUR, Lynne
; APPLICANT: CUELLO, Claudio A.
; TITLE OF INVENTION: NERVE GROWTH FACTOR STRUCTURAL ANALOGS
; TITLE OF INVENTION: AND THEIR USES
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: KLAUBER & JACKSON

```

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; STREET: Continental Plaza, 411 Hackensack Avenue
; CITY: Hackensack
; STATE: N.J.
; COUNTRY: U.S.A.
; ZIP: 07601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/696,854B
; FILING DATE: 07-AUG-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO PCT/CA95/00059
; FILING DATE: 07-FEB-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9402331.4
; FILING DATE: 07-FEB-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: JACKSON, David A.
; REGISTRATION NUMBER: 26,742
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (201) 487-5800
; TELEFAX: (201) 343-1684
; TELEX: 133521
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: one-of (1, 11)
; OTHER INFORMATION: /note= "Xaa is any uncharged amino acid
; OTHER INFORMATION: or hydrophatic amino acid"
US-08-696-854B-3

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Query Match          36.4%; Score 4; DB 3; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches      4; Conservative      0; Mismatches      0; Indels      0; Gaps      0;

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Qy      8 TAIK 11
        ||||
Db      3 TAIK 6

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RESULT 4
US-09-576-824A-547
; Sequence 547, Application US/09576824A
; Patent No. 6667387
; GENERAL INFORMATION:
; APPLICANT: De Leys, Robert
; TITLE OF INVENTION: PROCESS FOR THE DETERMINATION OF PEPTIDES CORRESPONDING
; TITLE OF INVENTION: TO IMMUNOLOGICALLY IMPORTANT EPITOPES AND THEIR USE IN

```

```

; TITLE OF INVENTION: A PROCESS FOR DETERMINATION OF ANTIBODIES OF
; TITLE OF INVENTION: BIOTINYLATED PEPTIDES CORRESPONDING TO IMMUNOLOGICALLY
IMPORTANT
; TITLE OF INVENTION: EPITOPES, A PROCESS FOR PREPARING THEM AND COMPOSITIONS
; TITLE OF INVENTION: CONTAINING THEM
; FILE REFERENCE: 2752-11
; CURRENT APPLICATION NUMBER: US/09/576,824A
; CURRENT FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 08/723,425
; PRIOR FILING DATE: 1996-09-30
; PRIOR APPLICATION NUMBER: 09/146,028
; PRIOR FILING DATE: 1993-11-22
; PRIOR APPLICATION NUMBER: PCT/EP93/00517
; PRIOR FILING DATE: 1993-03-08
; PRIOR APPLICATION NUMBER: EP 92400598.6
; PRIOR FILING DATE: 1992-03-06
; NUMBER OF SEQ ID NOS: 600
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 547
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Hepatitis C virus
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; NAME/KEY: VARIANT
; LOCATION: (1)
; OTHER INFORMATION: Xaa = modified site : when present, represents an
; OTHER INFORMATION: amino acid, amino group, or chemically modified
; OTHER INFORMATION: amino terminus
; NAME/KEY: VARIANT
; LOCATION: (11)
; OTHER INFORMATION: Xaa = modified site : when present, represents an
; OTHER INFORMATION: amino acid, OH-group, NH2-group, or a linkage
; OTHER INFORMATION: involv-ing these two groups
US-09-576-824A-547

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Query Match          36.4%; Score 4; DB 4; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches      4; Conservative      0; Mismatches      0; Indels      0; Gaps      0;

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Qy      2 RKSR 5
      ||||
Db      7 RKSR 10

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# RESULT 5

US-09-576-824A-548

; Sequence 548, Application US/09576824A

; Patent No. 6667387

; GENERAL INFORMATION:

; APPLICANT: De Leys, Robert

; TITLE OF INVENTION: PROCESS FOR THE DETERMINATION OF PEPTIDES CORRESPONDING

; TITLE OF INVENTION: TO IMMUNOLOGICALLY IMPORTANT EPITOPES AND THEIR USE IN

; TITLE OF INVENTION: A PROCESS FOR DETERMINATION OF ANTIBODIES OF

; TITLE OF INVENTION: BIOTINYLATED PEPTIDES CORRESPONDING TO IMMUNOLOGICALLY  
IMPORTANT

; TITLE OF INVENTION: EPITOPES, A PROCESS FOR PREPARING THEM AND COMPOSITIONS

; TITLE OF INVENTION: CONTAINING THEM

```

; FILE REFERENCE: 2752-11
; CURRENT APPLICATION NUMBER: US/09/576,824A
; CURRENT FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 08/723,425
; PRIOR FILING DATE: 1996-09-30
; PRIOR APPLICATION NUMBER: 09/146,028
; PRIOR FILING DATE: 1993-11-22
; PRIOR APPLICATION NUMBER: PCT/EP93/00517
; PRIOR FILING DATE: 1993-03-08
; PRIOR APPLICATION NUMBER: EP 92400598.6
; PRIOR FILING DATE: 1992-03-06
; NUMBER OF SEQ ID NOS: 600
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 548
;   LENGTH: 11
;   TYPE: PRT
;   ORGANISM: Hepatitis C virus
;   FEATURE:
;   NAME/KEY: VARIANT
;   LOCATION: (1)
;   OTHER INFORMATION: Xaa = modified site : when present, represents an
;   OTHER INFORMATION: amino acid, amino group, or chemically modified
;   OTHER INFORMATION: amino terminus
;   NAME/KEY: VARIANT
;   LOCATION: (11)
;   OTHER INFORMATION: Xaa = modified site : when present, represents an
;   OTHER INFORMATION: amino acid, OH-group, NH2-group, or a linkage
;   OTHER INFORMATION: involv-ing these two groups
US-09-576-824A-548

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Query Match          36.4%; Score 4; DB 4; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches      4; Conservative      0; Mismatches      0; Indels      0; Gaps      0;

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Qy      2 RKSR 5
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Db      6 RKSR 9

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# RESULT 6

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US-09-576-824A-549
; Sequence 549, Application US/09576824A
; Patent No. 6667387
; GENERAL INFORMATION:
; APPLICANT: De Leys, Robert
; TITLE OF INVENTION: PROCESS FOR THE DETERMINATION OF PEPTIDES CORRESPONDING
; TITLE OF INVENTION: TO IMMUNOLOGICALLY IMPORTANT EPITOPES AND THEIR USE IN
; TITLE OF INVENTION: A PROCESS FOR DETERMINATION OF ANTIBODIES OF
; TITLE OF INVENTION: BIOTINYLATED PEPTIDES CORRESPONDING TO IMMUNOLOGICALLY
IMPORTANT
; TITLE OF INVENTION: EPITOPES, A PROCESS FOR PREPARING THEM AND COMPOSITIONS
; TITLE OF INVENTION: CONTAINING THEM
; FILE REFERENCE: 2752-11
; CURRENT APPLICATION NUMBER: US/09/576,824A
; CURRENT FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 08/723,425
; PRIOR FILING DATE: 1996-09-30

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; PRIOR APPLICATION NUMBER: 09/146,028
; PRIOR FILING DATE: 1993-11-22
; PRIOR APPLICATION NUMBER: PCT/EP93/00517
; PRIOR FILING DATE: 1993-03-08
; PRIOR APPLICATION NUMBER: EP 92400598.6
; PRIOR FILING DATE: 1992-03-06
; NUMBER OF SEQ ID NOS: 600
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 549
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Hepatitis C virus
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: (1)
; OTHER INFORMATION: Xaa = modified site : when present, represents an
; OTHER INFORMATION: amino acid, amino group, or chemically modified
; OTHER INFORMATION: amino terminus
; NAME/KEY: VARIANT
; LOCATION: (11)
; OTHER INFORMATION: Xaa = modified site : when present, represents an
; OTHER INFORMATION: amino acid, OH-group, NH2-group, or a linkage
; OTHER INFORMATION: involv-ing these two groups
US-09-576-824A-549

```

```

Query Match          36.4%; Score 4; DB 4; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches      4; Conservative      0; Mismatches      0; Indels      0; Gaps      0;

```

```

Qy      2 RKSR 5
        ||||
Db      5 RKSR 8

```

# RESULT 7

```

PCT-US91-08328-13
; Sequence 13, Application PC/TUS9108328
; GENERAL INFORMATION:
; APPLICANT: Ruggeri, Zaverio M.
; APPLICANT: Houghten, Richard A.
; TITLE OF INVENTION: PEPTIDES THAT INHIBIT PLATELET BINDING
; TITLE OF INVENTION: OF ADHESION MOLECULES
; NUMBER OF SEQUENCES: 47
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Eugene Moroz, MORGAN & FINNEGAN
; STREET: 345 Park Avenue
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10154
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US91/08328

```

```

; FILING DATE: 19911107
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/610,363
; FILING DATE: 07-NOV-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Moroz, Eugene
; REGISTRATION NUMBER: 25,237
; REFERENCE/DOCKET NUMBER: 1198 4079PC
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212)758-4800
; TELEFAX: (212)751-6849
; TELEX: 421792
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: AMINO ACID
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FEATURE:
; NAME/KEY: Cross-links
; LOCATION: 6..>11
; OTHER INFORMATION: /note= "Sequence linked by
; OTHER INFORMATION: interchain amide bond at Lys residue with Glu
; OTHER INFORMATION: residue on Arg5-Glu-Ser-Arg-Gly-Asp-Val sequence"
; PUBLICATION INFORMATION:
; DOCUMENT NUMBER: US 4,683,291
; FILING DATE: 28-OCT-1985
; PUBLICATION DATE: 28-JUL-1987
; PUBLICATION INFORMATION:
; DOCUMENT NUMBER: US B1 4,683,291
; FILING DATE: 28-OCT-1985
; PUBLICATION DATE: 03-JUL-1990
PCT-US91-08328-13

```

```

Query Match          36.4%; Score 4; DB 5; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches      4; Conservative      0; Mismatches      0; Indels      0; Gaps      0;

```

```

Qy      2 RKSR 5
        ||||
Db      5 RKSR 8

```

```

RESULT 8
US-07-851-941-12
; Sequence 12, Application US/07851941
; Patent No. 5428016
; GENERAL INFORMATION:
; APPLICANT: Mamoru TOMITA et al.
; TITLE OF INVENTION: Antimicrobial Peptide and an
; TITLE OF INVENTION: Antimicrobial Agent
; NUMBER OF SEQUENCES: 18
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Wenderoth, Lind & Ponack

```

;  
; STREET: 805 Fifteenth Street, N.W., #700  
;  
; CITY: Washington  
;  
; STATE: D.C.  
;  
; COUNTRY: U.S.A.  
;  
; ZIP: 20005  
;  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette, 5.25 inch, 500 kb  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: MS-DOS  
; SOFTWARE: DisplayWrite  
;  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/07/851,941  
; FILING DATE: 19920313  
; CLASSIFICATION: 530  
;  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 07/851,941  
; FILING DATE: March 13, 1992  
;  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Warren M. Cheek, Jr.  
; REGISTRATION NUMBER: 33,367  
; REFERENCE/DOCKET NUMBER:  
;  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 202-371-8850  
; TELEFAX:  
; TELEX:  
;  
; INFORMATION FOR SEQ ID NO: 12:  
;  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 11 amino acid residues  
; TYPE: AMINO ACID  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
;  
; MOLECULE TYPE: peptide  
;  
; HYPOTHETICAL:  
;  
; ANTI-SENSE:  
;  
; FRAGMENT TYPE:  
;  
; ORIGINAL SOURCE:  
;  
; ORGANISM:  
;  
; STRAIN:  
;  
; INDIVIDUAL ISOLATE:  
;  
; DEVELOPMENTAL STAGE:  
;  
; HAPLOTYPE:  
;  
; TISSUE TYPE:  
;  
; CELL TYPE:  
;  
; CELL LINE:  
;  
; ORGANELLE:  
;  
; IMMEDIATE SOURCE:  
;  
; LIBRARY:  
;  
; CLONE:  
;  
; POSITION IN GENOME:  
;  
; CHROMOSOME/SEGMENT:  
;  
; MAP POSITION:  
;  
; UNITS:  
;  
; FEATURE:  
;  
; NAME/KEY:  
;  
; LOCATION:  
;  
; IDENTIFICATION METHOD:  
;  
; OTHER INFORMATION:

; PUBLICATION INFORMATION:  
;  
; AUTHORS:  
;  
; TITLE:  
;  
; JOURNAL:  
;  
; VOLUME:  
;  
; ISSUE:  
;  
; PAGES:  
;  
; DATE:  
;  
; DOCUMENT NUMBER:  
;  
; FILING DATE:  
;  
; PUBLICATION DATE:  
;  
; RELEVANT RESIDUES IN SEQ ID NO:  
US-07-851-941-12

Query Match 27.3%; Score 3; DB 1; Length 11;  
Best Local Similarity 100.0%; Pred. No. 1.8e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 KSR 5  
|||  
Db 1 KSR 3

RESULT 9

US-08-197-795-5

; Sequence 5, Application US/08197795  
; Patent No. 5457182  
; GENERAL INFORMATION:  
; APPLICANT: Wiederrecht, Gregory J.  
; APPLICANT: Sewell, Tonya J.  
; TITLE OF INVENTION: FK-506 CYTOSOLIC BINDING PROTEIN  
; NUMBER OF SEQUENCES: 21  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Merck & Co., Inc.  
; STREET: 126 E. Lincoln Avenue  
; CITY: Rahway  
; STATE: New Jersey  
; COUNTRY: USA  
; ZIP: 07065  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/197,795  
; FILING DATE:  
; CLASSIFICATION: 530  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Thies, J. Eric  
; REGISTRATION NUMBER: 35,382  
; REFERENCE/DOCKET NUMBER: 19181  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (908) 594-3904  
; TELEFAX: (908) 594-4720  
; INFORMATION FOR SEQ ID NO: 5:  
; SEQUENCE CHARACTERISTICS:



; LENGTH: 11 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; HYPOTHETICAL: NO  
; ANTI-SENSE: NO  
US-08-197-795-5

Query Match 27.3%; Score 3; DB 1; Length 11;  
Best Local Similarity 100.0%; Pred. No. 1.8e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 SRD 6  
|||  
Db 2 SRD 4

RESULT 10

US-08-431-539-10

; Sequence 10, Application US/08431539

; Patent No. 5580751

; GENERAL INFORMATION:

; APPLICANT: Buchardt, Ole

; APPLICANT: Breddam, Klaus

; APPLICANT: Henriksen, Dennis

; TITLE OF INVENTION: Process for the Preparation of

; TITLE OF INVENTION: C-Terminally Amidated Peptides

; NUMBER OF SEQUENCES: 19

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Merchant & Gould

; STREET: 3100 No. 5580751west Center

; CITY: Minneapolis

; STATE: MN

; COUNTRY: USA

; ZIP: 55402

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/431,539

; FILING DATE:

; CLASSIFICATION: 435

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 08/039,306

; FILING DATE: 15-APR-1993

; ATTORNEY/AGENT INFORMATION:

; NAME: Nelson, Albin J.

; REGISTRATION NUMBER: 28,650

; REFERENCE/DOCKET NUMBER: 9663.8-US-WO

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 612-332-5300

; TELEFAX: 612-332-9081

; INFORMATION FOR SEQ ID NO: 10:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 11 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
US-08-431-539-10

Query Match 27.3%; Score 3; DB 1; Length 11;  
Best Local Similarity 100.0%; Pred. No. 1.8e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 TAI 10  
|||  
Db 3 TAI 5

RESULT 11

US-08-431-539-16

; Sequence 16, Application US/08431539  
; Patent No. 5580751  
; GENERAL INFORMATION:  
; APPLICANT: Buchardt, Ole  
; APPLICANT: Breddam, Klaus  
; APPLICANT: Henriksen, Dennis  
; TITLE OF INVENTION: Process for the Preparation of  
; TITLE OF INVENTION: C-Terminally Amidated Peptides  
; NUMBER OF SEQUENCES: 19  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Merchant & Gould  
; STREET: 3100 No. 5580751west Center  
; CITY: Minneapolis  
; STATE: MN  
; COUNTRY: USA  
; ZIP: 55402  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/431,539  
; FILING DATE:  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/039,306  
; FILING DATE: 15-APR-1993  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Nelson, Albin J.  
; REGISTRATION NUMBER: 28,650  
; REFERENCE/DOCKET NUMBER: 9663.8-US-WO  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 612-332-5300  
; TELEFAX: 612-332-9081  
; INFORMATION FOR SEQ ID NO: 16:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 11 amino acids  
; TYPE: amino acid

; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
US-08-431-539-16

Query Match 27.3%; Score 3; DB 1; Length 11;  
Best Local Similarity 100.0%; Pred. No. 1.8e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 TAI 10  
|||  
Db 3 TAI 5

RESULT 12

US-08-615-181-84

; Sequence 84, Application US/08615181

; Patent No. 5756666

; GENERAL INFORMATION:

; APPLICANT: MASAFUMI, TAKIGUCHI

; APPLICANT: MIWA, KIYOSHI

; TITLE OF INVENTION: PEPTIDES CAPABLE OF INDUCING IMMUNE

; TITLE OF INVENTION: RESPONSE TO HIV AND ANTI-AIDS AGENT FOR PREVENTING AND

; TITLE OF INVENTION: CURING AIDS

; NUMBER OF SEQUENCES: 115

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,

; ADDRESSEE: P.C.

; STREET: 1755 S. JEFFERSON DAVIS HIGHWAY, SUITE 400

; CITY: ARLINGTON

; STATE: VA

; COUNTRY: USA

; ZIP: 22202

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/615,181

; FILING DATE: 04-APR-1996

; CLASSIFICATION: 424

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: PCT/JP94/01756

; FILING DATE: 19-OCT-1994

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: JP 261302/1993

; FILING DATE: 19-OCT-1993

; ATTORNEY/AGENT INFORMATION:

; NAME: OBLON, NORMAN F.

; REGISTRATION NUMBER: 24,618

; REFERENCE/DOCKET NUMBER: 10-796-0 PCT

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 703-413-3000

; TELEFAX: 703-413-2220

; INFORMATION FOR SEQ ID NO: 84:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 11 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
; ORIGINAL SOURCE:  
; ORGANISM: HUMAN IMMUNODEFICIENCY VIRUS  
US-08-615-181-84

Query Match 27.3%; Score 3; DB 1; Length 11;  
Best Local Similarity 100.0%; Pred. No. 1.8e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 RKS 4  
|||  
Db 7 RKS 9

RESULT 13

US-08-456-670B-28

; Sequence 28, Application US/08456670B  
; Patent No. 5932415

; GENERAL INFORMATION:

; APPLICANT: SCHUBERT, PETER  
; APPLICANT: NEUMANN, SIEGFRIED  
; APPLICANT: PAWELZIK, MARTINA  
; APPLICANT: LINXWEILER, WINFRIED  
; APPLICANT: BURGER, CHRISTA  
; APPLICANT: HOFMANN, GOTTFRIED  
; APPLICANT: BUBERT, ANDREAS  
; APPLICANT: GOEBEL, WERNER  
; APPLICANT: KOHLER, STEFAN

; TITLE OF INVENTION: PROCESSES AND AGENTS FOR DETECTING

; TITLE OF INVENTION: LISTERIAS

; NUMBER OF SEQUENCES: 43

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: MILLEN, WHITE, ZELANO & BRANIGAN, P.C.  
; STREET: 2200 CLARENDON BLVD., SUITE 1400  
; CITY: ARLINGTON  
; STATE: VIRGINIA  
; COUNTRY: US  
; ZIP: 22201

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/456,670B  
; FILING DATE: 01-JUN-1995  
; CLASSIFICATION: 435

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 08/412,227  
; FILING DATE: 27-MAR-1995

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 08/075,248  
; FILING DATE: 11-JUN-1993

```

; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: DE 4239567.4
; FILING DATE: 25-NOV-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: DE 4219111.4
; FILING DATE: 11-JUN-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: HAMLET-KING, DIANA
; REGISTRATION NUMBER: 33,302
; REFERENCE/DOCKET NUMBER: MERCK 1694D1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703-243-6333
; TELEFAX: 703-243-6410
; TELEX: 64191
; INFORMATION FOR SEQ ID NO: 28:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; ORIGINAL SOURCE:
; ORGANISM: Listeria monocytogenes
; STRAIN: EGD
US-08-456-670B-28

```

```

Query Match          27.3%; Score 3; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches      3; Conservative      0; Mismatches      0; Indels      0; Gaps      0;

```

```

Qy          9 AIK 11
            |||
Db          2 AIK 4

```

# RESULT 14

```

US-08-350-260A-340
; Sequence 340, Application US/08350260A
; Patent No. 5962255
; GENERAL INFORMATION:
; APPLICANT: Winter, Gregory Paul
; APPLICANT: Griffiths, Andrew David
; APPLICANT: Williams, Samuel Cameron
; APPLICANT: Waterhouse, Peter
; APPLICANT: Nissim, Ahuva
; APPLICANT: Johnson, Kevin Stuart
; APPLICANT: Smith, Andrew John Hammond
; TITLE OF INVENTION: Methods for producing members of specific
; TITLE OF INVENTION: binding pairs
; NUMBER OF SEQUENCES: 602
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: David W. Clough
; STREET: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 6300 Sears Tower, 233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606-6402

```

```

; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/350,260A
; FILING DATE: 05-DEC-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9110549.4
; FILING DATE: 15-MAY-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9206318.9
; FILING DATE: 24-MAR-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/GB91/01134
; FILING DATE: 10-JUL-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/GB92/00883
; FILING DATE: 15-MAY-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/GB93/00605
; FILING DATE: 24-MAR-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/150,002
; FILING DATE: 31-MAR-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/307,619
; FILING DATE: 16-SEP-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Clough, David W
; REGISTRATION NUMBER: 36,107
; REFERENCE/DOCKET NUMBER: 28111/32372
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312-474-6300
; INFORMATION FOR SEQ ID NO: 340:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-350-260A-340

```

```

Query Match          27.3%; Score 3; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches      3; Conservative      0; Mismatches      0; Indels      0; Gaps      0;

```

```

Qy      4 SRD 6
      |||
Db      2 SRD 4

```

```

RESULT 15
US-08-350-260A-342
; Sequence 342, Application US/08350260A
; Patent No. 5962255

```

; GENERAL INFORMATION:  
; APPLICANT: Winter, Gregory Paul  
; APPLICANT: Griffiths, Andrew David  
; APPLICANT: Williams, Samuel Cameron  
; APPLICANT: Waterhouse, Peter  
; APPLICANT: Nissim, Ahuva  
; APPLICANT: Johnson, Kevin Stuart  
; APPLICANT: Smith, Andrew John Hammond  
; TITLE OF INVENTION: Methods for producing members of specific  
; TITLE OF INVENTION: binding pairs  
; NUMBER OF SEQUENCES: 602  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: David W. Clough  
; STREET: Marshall, O'Toole, Gerstein, Murray & Borun  
; STREET: 6300 Sears Tower, 233 South Wacker Drive  
; CITY: Chicago  
; STATE: Illinois  
; COUNTRY: USA  
; ZIP: 60606-6402  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/350,260A  
; FILING DATE: 05-DEC-1994  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: GB 9110549.4  
; FILING DATE: 15-MAY-1991  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: GB 9206318.9  
; FILING DATE: 24-MAR-1992  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: PCT/GB91/01134  
; FILING DATE: 10-JUL-1991  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: PCT/GB92/00883  
; FILING DATE: 15-MAY-1992  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: PCT/GB93/00605  
; FILING DATE: 24-MAR-1993  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/150,002  
; FILING DATE: 31-MAR-1994  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/307,619  
; FILING DATE: 16-SEP-1994  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Clough, David W  
; REGISTRATION NUMBER: 36,107  
; REFERENCE/DOCKET NUMBER: 28111/32372  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 312-474-6300  
; INFORMATION FOR SEQ ID NO: 342:  
; SEQUENCE CHARACTERISTICS:

; LENGTH: 11 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
US-08-350-260A-342

Query Match 27.3%; Score 3; DB 2; Length 11;  
Best Local Similarity 100.0%; Pred. No. 1.8e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 SRD 6  
|||  
Db 2 SRD 4

RESULT 16

US-08-350-260A-349

; Sequence 349, Application US/08350260A  
; Patent No. 5962255  
; GENERAL INFORMATION:  
; APPLICANT: Winter, Gregory Paul  
; APPLICANT: Griffiths, Andrew David  
; APPLICANT: Williams, Samuel Cameron  
; APPLICANT: Waterhouse, Peter  
; APPLICANT: Nissim, Ahuva  
; APPLICANT: Johnson, Kevin Stuart  
; APPLICANT: Smith, Andrew John Hammond  
; TITLE OF INVENTION: Methods for producing members of specific  
; TITLE OF INVENTION: binding pairs  
; NUMBER OF SEQUENCES: 602  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: David W. Clough  
; STREET: Marshall, O'Toole, Gerstein, Murray & Borun  
; STREET: 6300 Sears Tower, 233 South Wacker Drive  
; CITY: Chicago  
; STATE: Illinois  
; COUNTRY: USA  
; ZIP: 60606-6402  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/350,260A  
; FILING DATE: 05-DEC-1994  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: GB 9110549.4  
; FILING DATE: 15-MAY-1991  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: GB 9206318.9  
; FILING DATE: 24-MAR-1992  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: PCT/GB91/01134  
; FILING DATE: 10-JUL-1991  
; PRIOR APPLICATION DATA:



```

; APPLICATION NUMBER: PCT/GB92/00883
; FILING DATE: 15-MAY-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/GB93/00605
; FILING DATE: 24-MAR-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/150,002
; FILING DATE: 31-MAR-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/307,619
; FILING DATE: 16-SEP-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Clough, David W
; REGISTRATION NUMBER: 36,107
; REFERENCE/DOCKET NUMBER: 28111/32372
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312-474-6300
; INFORMATION FOR SEQ ID NO: 349:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-350-260A-349

```

```

Query Match          27.3%; Score 3; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches      3; Conservative      0; Mismatches      0; Indels      0; Gaps      0;

```

```

Qy      4 SRD 6
      |||
Db      2 SRD 4

```

# RESULT 17

US-08-350-260A-375

```

; Sequence 375, Application US/08350260A
; Patent No. 5962255

```

## ; GENERAL INFORMATION:

```

; APPLICANT: Winter, Gregory Paul
; APPLICANT: Griffiths, Andrew David
; APPLICANT: Williams, Samuel Cameron
; APPLICANT: Waterhouse, Peter
; APPLICANT: Nissim, Ahuva
; APPLICANT: Johnson, Kevin Stuart
; APPLICANT: Smith, Andrew John Hammond
; TITLE OF INVENTION: Methods for producing members of specific
; TITLE OF INVENTION: binding pairs
; NUMBER OF SEQUENCES: 602
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: David W. Clough
; STREET: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 6300 Sears Tower, 233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606-6402

```

```

; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/350,260A
; FILING DATE: 05-DEC-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9110549.4
; FILING DATE: 15-MAY-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9206318.9
; FILING DATE: 24-MAR-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/GB91/01134
; FILING DATE: 10-JUL-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/GB92/00883
; FILING DATE: 15-MAY-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/GB93/00605
; FILING DATE: 24-MAR-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/150,002
; FILING DATE: 31-MAR-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/307,619
; FILING DATE: 16-SEP-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Clough, David W
; REGISTRATION NUMBER: 36,107
; REFERENCE/DOCKET NUMBER: 28111/32372
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312-474-6300
; INFORMATION FOR SEQ ID NO: 375:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-350-260A-375

```

```

Query Match          27.3%; Score 3; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches      3; Conservative      0; Mismatches      0; Indels      0; Gaps      0;

```

```

Qy      4 SRD 6
      |||
Db      2 SRD 4

```

```

RESULT 18
US-08-350-260A-424
; Sequence 424, Application US/08350260A
; Patent No. 5962255

```

; GENERAL INFORMATION:  
; APPLICANT: Winter, Gregory Paul  
; APPLICANT: Griffiths, Andrew David  
; APPLICANT: Williams, Samuel Cameron  
; APPLICANT: Waterhouse, Peter  
; APPLICANT: Nissim, Ahuva  
; APPLICANT: Johnson, Kevin Stuart  
; APPLICANT: Smith, Andrew John Hammond  
; TITLE OF INVENTION: Methods for producing members of specific  
; TITLE OF INVENTION: binding pairs  
; NUMBER OF SEQUENCES: 602  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: David W. Clough  
; STREET: Marshall, O'Toole, Gerstein, Murray & Borun  
; STREET: 6300 Sears Tower, 233 South Wacker Drive  
; CITY: Chicago  
; STATE: Illinois  
; COUNTRY: USA  
; ZIP: 60606-6402  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/350,260A  
; FILING DATE: 05-DEC-1994  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: GB 9110549.4  
; FILING DATE: 15-MAY-1991  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: GB 9206318.9  
; FILING DATE: 24-MAR-1992  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: PCT/GB91/01134  
; FILING DATE: 10-JUL-1991  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: PCT/GB92/00883  
; FILING DATE: 15-MAY-1992  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: PCT/GB93/00605  
; FILING DATE: 24-MAR-1993  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/150,002  
; FILING DATE: 31-MAR-1994  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/307,619  
; FILING DATE: 16-SEP-1994  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Clough, David W  
; REGISTRATION NUMBER: 36,107  
; REFERENCE/DOCKET NUMBER: 28111/32372  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 312-474-6300  
; INFORMATION FOR SEQ ID NO: 424:  
; SEQUENCE CHARACTERISTICS:

; LENGTH: 11 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
US-08-350-260A-424

Query Match 27.3%; Score 3; DB 2; Length 11;  
Best Local Similarity 100.0%; Pred. No. 1.8e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 SRD 6  
|||  
Db 2 SRD 4

RESULT 19

US-08-350-260A-427

; Sequence 427, Application US/08350260A  
; Patent No. 5962255  
; GENERAL INFORMATION:  
; APPLICANT: Winter, Gregory Paul  
; APPLICANT: Griffiths, Andrew David  
; APPLICANT: Williams, Samuel Cameron  
; APPLICANT: Waterhouse, Peter  
; APPLICANT: Nissim, Ahuva  
; APPLICANT: Johnson, Kevin Stuart  
; APPLICANT: Smith, Andrew John Hammond  
; TITLE OF INVENTION: Methods for producing members of specific  
; TITLE OF INVENTION: binding pairs  
; NUMBER OF SEQUENCES: 602  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: David W. Clough  
; STREET: Marshall, O'Toole, Gerstein, Murray & Borun  
; STREET: 6300 Sears Tower, 233 South Wacker Drive  
; CITY: Chicago  
; STATE: Illinois  
; COUNTRY: USA  
; ZIP: 60606-6402  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/350,260A  
; FILING DATE: 05-DEC-1994  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: GB 9110549.4  
; FILING DATE: 15-MAY-1991  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: GB 9206318.9  
; FILING DATE: 24-MAR-1992  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: PCT/GB91/01134  
; FILING DATE: 10-JUL-1991  
; PRIOR APPLICATION DATA:

```

; APPLICATION NUMBER: PCT/GB92/00883
; FILING DATE: 15-MAY-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/GB93/00605
; FILING DATE: 24-MAR-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/150,002
; FILING DATE: 31-MAR-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/307,619
; FILING DATE: 16-SEP-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Clough, David W
; REGISTRATION NUMBER: 36,107
; REFERENCE/DOCKET NUMBER: 28111/32372
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312-474-6300
; INFORMATION FOR SEQ ID NO: 427:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-350-260A-427

```

```

Query Match          27.3%; Score 3; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches      3; Conservative      0; Mismatches      0; Indels      0; Gaps      0;

```

```

Qy      4 SRD 6
      |||
Db      2 SRD 4

```

# RESULT 20

US-08-350-260A-430

; Sequence 430, Application US/08350260A

; Patent No. 5962255

## ; GENERAL INFORMATION:

```

; APPLICANT: Winter, Gregory Paul
; APPLICANT: Griffiths, Andrew David
; APPLICANT: Williams, Samuel Cameron
; APPLICANT: Waterhouse, Peter
; APPLICANT: Nissim, Ahuva
; APPLICANT: Johnson, Kevin Stuart
; APPLICANT: Smith, Andrew John Hammond
; TITLE OF INVENTION: Methods for producing members of specific
; TITLE OF INVENTION: binding pairs
; NUMBER OF SEQUENCES: 602
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: David W. Clough
; STREET: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 6300 Sears Tower, 233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606-6402

```

```

; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/350,260A
; FILING DATE: 05-DEC-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9110549.4
; FILING DATE: 15-MAY-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9206318.9
; FILING DATE: 24-MAR-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/GB91/01134
; FILING DATE: 10-JUL-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/GB92/00883
; FILING DATE: 15-MAY-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/GB93/00605
; FILING DATE: 24-MAR-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/150,002
; FILING DATE: 31-MAR-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/307,619
; FILING DATE: 16-SEP-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Clough, David W
; REGISTRATION NUMBER: 36,107
; REFERENCE/DOCKET NUMBER: 28111/32372
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312-474-6300
; INFORMATION FOR SEQ ID NO: 430:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-350-260A-430

```

```

Query Match          27.3%; Score 3; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches      3; Conservative      0; Mismatches      0; Indels      0; Gaps      0;

```

```

Qy      4 SRD 6
      |||
Db      2 SRD 4

```

```

RESULT 21
US-08-350-260A-516
; Sequence 516, Application US/08350260A
; Patent No. 5962255

```

; GENERAL INFORMATION:  
;  
; APPLICANT: Winter, Gregory Paul  
; APPLICANT: Griffiths, Andrew David  
; APPLICANT: Williams, Samuel Cameron  
; APPLICANT: Waterhouse, Peter  
; APPLICANT: Nissim, Ahuva  
; APPLICANT: Johnson, Kevin Stuart  
; APPLICANT: Smith, Andrew John Hammond  
; TITLE OF INVENTION: Methods for producing members of specific  
; TITLE OF INVENTION: binding pairs  
; NUMBER OF SEQUENCES: 602  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: David W. Clough  
; STREET: Marshall, O'Toole, Gerstein, Murray & Borun  
; STREET: 6300 Sears Tower, 233 South Wacker Drive  
; CITY: Chicago  
; STATE: Illinois  
; COUNTRY: USA  
; ZIP: 60606-6402  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/350,260A  
; FILING DATE: 05-DEC-1994  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: GB 9110549.4  
; FILING DATE: 15-MAY-1991  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: GB 9206318.9  
; FILING DATE: 24-MAR-1992  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: PCT/GB91/01134  
; FILING DATE: 10-JUL-1991  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: PCT/GB92/00883  
; FILING DATE: 15-MAY-1992  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: PCT/GB93/00605  
; FILING DATE: 24-MAR-1993  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/150,002  
; FILING DATE: 31-MAR-1994  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/307,619  
; FILING DATE: 16-SEP-1994  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Clough, David W  
; REGISTRATION NUMBER: 36,107  
; REFERENCE/DOCKET NUMBER: 28111/32372  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 312-474-6300  
; INFORMATION FOR SEQ ID NO: 516:  
; SEQUENCE CHARACTERISTICS:

; LENGTH: 11 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
US-08-350-260A-516

Query Match 27.3%; Score 3; DB 2; Length 11;  
Best Local Similarity 100.0%; Pred. No. 1.8e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 SRD 6  
|||  
Db 2 SRD 4

RESULT 22

US-08-350-260A-522

; Sequence 522, Application US/08350260A

; Patent No. 5962255

; GENERAL INFORMATION:

; APPLICANT: Winter, Gregory Paul

; APPLICANT: Griffiths, Andrew David

; APPLICANT: Williams, Samuel Cameron

; APPLICANT: Waterhouse, Peter

; APPLICANT: Nissim, Ahuva

; APPLICANT: Johnson, Kevin Stuart

; APPLICANT: Smith, Andrew John Hammond

; TITLE OF INVENTION: Methods for producing members of specific

; TITLE OF INVENTION: binding pairs

; NUMBER OF SEQUENCES: 602

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: David W. Clough

; STREET: Marshall, O'Toole, Gerstein, Murray & Borun

; STREET: 6300 Sears Tower, 233 South Wacker Drive

; CITY: Chicago

; STATE: Illinois

; COUNTRY: USA

; ZIP: 60606-6402

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/350,260A

; FILING DATE: 05-DEC-1994

; CLASSIFICATION: 435

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: GB 9110549.4

; FILING DATE: 15-MAY-1991

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: GB 9206318.9

; FILING DATE: 24-MAR-1992

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: PCT/GB91/01134

; FILING DATE: 10-JUL-1991

; PRIOR APPLICATION DATA:



; APPLICATION NUMBER: PCT/GB92/00883  
 ; FILING DATE: 15-MAY-1992  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: PCT/GB93/00605  
 ; FILING DATE: 24-MAR-1993  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: US 08/150,002  
 ; FILING DATE: 31-MAR-1994  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: US 08/307,619  
 ; FILING DATE: 16-SEP-1994  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: Clough, David W  
 ; REGISTRATION NUMBER: 36,107  
 ; REFERENCE/DOCKET NUMBER: 28111/32372  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: 312-474-6300  
 ; INFORMATION FOR SEQ ID NO: 522:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 11 amino acids  
 ; TYPE: amino acid  
 ; STRANDEDNESS: single  
 ; TOPOLOGY: linear  
 US-08-350-260A-522

Query Match 27.3%; Score 3; DB 2; Length 11;  
 Best Local Similarity 100.0%; Pred. No. 1.8e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 SRD 6  
 |||  
 Db 2 SRD 4

# RESULT 23

US-08-751-767A-29

; Sequence 29, Application US/08751767A  
 ; Patent No. 5994104  
 ; GENERAL INFORMATION:  
 ; APPLICANT: ANDERSON, ROBERT J.  
 ; APPLICANT: GRANT, HUGH  
 ; APPLICANT: MACDONALD, IAN D.  
 ; TITLE OF INVENTION: INTERLUKIN-12 FUSION PROTEIN  
 ; NUMBER OF SEQUENCES: 80  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: NIXON & VANDERHYE P.C.  
 ; STREET: 1100 NORTH GLEBE ROAD  
 ; CITY: ARLINGTON  
 ; STATE: VA  
 ; COUNTRY: USA  
 ; ZIP: 22201  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: PatentIn Release #1.0, Version #1.30  
 ; CURRENT APPLICATION DATA:

```

; APPLICATION NUMBER: US/08/751,767A
; FILING DATE: 08-NOV-1996
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: SADOFF, B.J.
; REGISTRATION NUMBER: 36,663
; REFERENCE/DOCKET NUMBER: 117-221
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 7038164091
; TELEFAX: 7038164100
; INFORMATION FOR SEQ ID NO: 29:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-751-767A-29

```

```

Query Match          27.3%; Score 3; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches      3; Conservative      0; Mismatches      0; Indels      0; Gaps      0;

```

```

Qy      2 RKS 4
      |||
Db      2 RKS 4

```

```

RESULT 24
US-09-115-209-74
; Sequence 74, Application US/09115209
; Patent No. 5998375
; GENERAL INFORMATION:
; APPLICANT: Thogersen, Henning
; APPLICANT: Madsen, Kjeld
; APPLICANT: Olsen, Uffe B.
; APPLICANT: Johansen, Nils L.
; APPLICANT: Scheideler, Mark
; TITLE OF INVENTION: No. 5998375iceptin Analogues
; FILE REFERENCE: 5285.200-US
; CURRENT APPLICATION NUMBER: US/09/115,209
; CURRENT FILING DATE: 1998-07-14
; EARLIER APPLICATION NUMBER: 0867/97
; EARLIER FILING DATE: 1997-07-15
; EARLIER APPLICATION NUMBER: 60/052,862
; EARLIER FILING DATE: 1997-07-17
; NUMBER OF SEQ ID NOS: 76
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 74
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Human
; FEATURE:
; OTHER INFORMATION: Xaa at position 10 is Orn
US-09-115-209-74

```

```

Query Match          27.3%; Score 3; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;

```

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ARK 3  
|||  
Db 7 ARK 9

RESULT 25

US-08-817-926-6

; Sequence 6, Application US/08817926

; Patent No. 6001590

; GENERAL INFORMATION:

; APPLICANT: Komeda, Toshihiro

; APPLICANT: Suda, Hisako

; APPLICANT: Tamai, Yukio

; APPLICANT: Iwamatsu, Akihiro

; APPLICANT: Kato, No. 6001590uo

; APPLICANT: Sakai, Yasuyoshi

; TITLE OF INVENTION: PROMOTER/TERMINATOR FOR CANDIDA BOIDINII

; TITLE OF INVENTION: FORMATE DEHYDROGENASE GENE

; NUMBER OF SEQUENCES: 51

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Foley & Lardner

; STREET: 3000 K Street, N.W., Suite 500

; CITY: Washington

; STATE: D.C.

; COUNTRY: USA

; ZIP: 20007-5109

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/817,926

; FILING DATE: 09-MAY-1997

; CLASSIFICATION: 435

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: PCT/JP96/02597

; FILING DATE: 12-SEP-1996

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: JP 234133/1995

; FILING DATE: 12-SEP-1995

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: JP 42536/1996

; FILING DATE: 29-FEB-1996

; ATTORNEY/AGENT INFORMATION:

; NAME: Bent, Stephen A.

; REGISTRATION NUMBER: 29,768

; REFERENCE/DOCKET NUMBER: 081356/0112

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (202)672-5300

; TELEFAX: (202)672-5399

; TELEX: 904136

; INFORMATION FOR SEQ ID NO: 6:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 11 amino acids

; TYPE: amino acid  
;  
; STRANDEDNESS:  
;  
; TOPOLOGY: linear  
;  
; MOLECULE TYPE: peptide  
US-08-817-926-6

Query Match 27.3%; Score 3; DB 3; Length 11;  
Best Local Similarity 100.0%; Pred. No. 1.8e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 RDM 7  
|||  
Db 6 RDM 8

RESULT 26

US-08-746-160-51

; Sequence 51, Application US/08746160  
; Patent No. 6010876  
; GENERAL INFORMATION:  
; APPLICANT: Lehrer, Robert I.  
; APPLICANT: Harwig, Sylvia L.  
; APPLICANT: Zhao, Chengquan  
; APPLICANT: Lee, In-Hee  
; TITLE OF INVENTION: CLAVANINS  
; NUMBER OF SEQUENCES: 51  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: MORRISON & FOERSTER  
; STREET: 2000 Pennsylvania Avenue, NW, suite 5500  
; CITY: Washington  
; STATE: DC  
; COUNTRY: USA  
; ZIP: 20006-1888  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: DOS  
; SOFTWARE: FastSEQ for Windows Version 2.0  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/746,160  
; FILING DATE: 06-NOV-1996  
; CLASSIFICATION: 530  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER:  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Murashige, Kate H  
; REGISTRATION NUMBER: 29,959  
; REFERENCE/DOCKET NUMBER: 22000-20563.00  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 202-887-1500  
; TELEFAX: 202-822-0168  
; TELEX:  
; INFORMATION FOR SEQ ID NO: 51:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 11 amino acids  
; TYPE: amino acid

; STRANDEDNESS: single  
; TOPOLOGY: linear  
US-08-746-160-51

Query Match 27.3%; Score 3; DB 3; Length 11;  
Best Local Similarity 100.0%; Pred. No. 1.8e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 RKS 4  
|||  
Db 5 RKS 7

RESULT 27

US-08-810-324-46  
; Sequence 46, Application US/08810324C  
; Patent No. 6040293  
; GENERAL INFORMATION:  
; APPLICANT: LEHRER, Robert I  
; APPLICANT: ZHAO, Chengquan  
; APPLICANT: LEE, In-Hee  
; APPLICANT: HARWIG, Sylvia L.  
; TITLE OF INVENTION: CLAVANINS  
; FILE REFERENCE: 22000-20563.20  
; CURRENT APPLICATION NUMBER: US/08/810,324C  
; CURRENT FILING DATE: 1997-02-28  
; EARLIER APPLICATION NUMBER: 08/746,160  
; EARLIER FILING DATE: 1996-11-06  
; NUMBER OF SEQ ID NOS: 52  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 46  
; LENGTH: 11  
; TYPE: PRT  
; ORGANISM: Styela clava  
US-08-810-324-46

Query Match 27.3%; Score 3; DB 3; Length 11;  
Best Local Similarity 100.0%; Pred. No. 1.8e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 RKS 4  
|||  
Db 5 RKS 7

RESULT 28

US-08-679-006-16  
; Sequence 16, Application US/08679006  
; Patent No. 6150500  
; GENERAL INFORMATION:  
; APPLICANT: Salerno, John C.  
; TITLE OF INVENTION: APPLICATIONS FOR REGULATORY REGION OF  
; TITLE OF INVENTION: NOS ISOFORMS  
; NUMBER OF SEQUENCES: 35  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.  
; STREET: Two Militia Drive

```

; CITY: Lexington
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02173
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/679,006
; FILING DATE: 12-JUL-1996
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Brook, David E.
; REGISTRATION NUMBER: 22,592
; REFERENCE/DOCKET NUMBER: JCS96-01
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 861-6240
; TELEFAX: (617) 861-9540
; INFORMATION FOR SEQ ID NO: 16:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-679-006-16

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```

Query Match          27.3%; Score 3; DB 3; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches      3; Conservative      0; Mismatches      0; Indels      0; Gaps      0;

```

```

Qy      2 RKS 4
      |||
Db      4 RKS 6

```

# RESULT 29

US-09-183-217-9

```

; Sequence 9, Application US/09183217A
; Patent No. 6153194
; GENERAL INFORMATION:
; APPLICANT: Skare, Jonathan T.
; APPLICANT: Shang, Ellen S.
; APPLICANT: Champion, Cheryl I.
; APPLICANT: Blanco, David R.
; APPLICANT: Miller, James N.
; APPLICANT: Lovett, Michael A.
; APPLICANT: Mizabekov, Tajib A.
; APPLICANT: Kagan, Bruce L.
; APPLICANT: Tempst, Paul
; APPLICANT: Foley, Denise M.
; TITLE OF INVENTION: BORRELIA BURGDORFERI OUTER MEMBRANE PROTEINS
; FILE REFERENCE: UC Case No. 6153194 96-059-3/Skare et al.
; CURRENT APPLICATION NUMBER: US/09/183,217A
; CURRENT FILING DATE: 1998-10-29

```

; PRIOR APPLICATION NUMBER: 08/787,367  
; PRIOR FILING DATE: 1997-01-22  
; NUMBER OF SEQ ID NOS: 9  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 9  
; LENGTH: 11  
; TYPE: PRT  
; ORGANISM: Borrelia burgdorferi  
US-09-183-217-9

Query Match 27.3%; Score 3; DB 3; Length 11;  
Best Local Similarity 100.0%; Pred. No. 1.8e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 AIK 11  
|||  
Db 9 AIK 11

RESULT 30  
US-09-206-059-4  
; Sequence 4, Application US/09206059  
; Patent No. 6201104  
; GENERAL INFORMATION:  
; APPLICANT: MacDonald, Nicholas  
; APPLICANT: Sim, Kim Lee  
; TITLE OF INVENTION: Angiogenesis-Inhibiting Protein Binding Peptides and  
; TITLE OF INVENTION: Proteins and Methods of Use  
; FILE REFERENCE: 05213-0370  
; CURRENT APPLICATION NUMBER: US/09/206,059  
; CURRENT FILING DATE: 1998-12-04  
; NUMBER OF SEQ ID NOS: 80  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 4  
; LENGTH: 11  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: synthetic  
; OTHER INFORMATION: binding peptides  
US-09-206-059-4

Query Match 27.3%; Score 3; DB 3; Length 11;  
Best Local Similarity 100.0%; Pred. No. 1.8e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 AIK 11  
|||  
Db 5 AIK 7

RESULT 31  
US-09-208-966-3  
; Sequence 3, Application US/09208966  
; Patent No. 6221355  
; GENERAL INFORMATION:  
; APPLICANT: Dowdy, Steven F.

```
; TITLE OF INVENTION: ANTI-PATHOGEN SYSTEM AND METHODS OF USE THEREOF
; FILE REFERENCE: 48881/1742
; CURRENT APPLICATION NUMBER: US/09/208,966
; CURRENT FILING DATE: 1998-12-10
; EARLIER APPLICATION NUMBER: 60/082,402
; EARLIER FILING DATE: 1998-04-20
; EARLIER APPLICATION NUMBER: 60/069,012
; EARLIER FILING DATE: 1997-12-10
; NUMBER OF SEQ ID NOS: 57
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3
; LENGTH: 11
; TYPE: PRT
; ORGANISM: human
US-09-208-966-3
```

```
Query Match          27.3%; Score 3; DB 3; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches      3; Conservative      0; Mismatches      0; Indels      0; Gaps      0;
```

```
Qy      1 ARK 3
        |||
Db      2 ARK 4
```

# RESULT 32

US-08-647-405B-3

```
; Sequence 3, Application US/08647405B
; Patent No. 6228654
; GENERAL INFORMATION:
; APPLICANT: Chait, Brian T.
; APPLICANT: Zhao, Yingming
; APPLICANT: Kent, Stephen B.H.
; TITLE OF INVENTION: METHODS FOR STRUCTURE ANALYSIS OF OLIGOSACCHARIDES
; FILE REFERENCE: Oligosaccharides
; CURRENT APPLICATION NUMBER: US/08/647,405B
; CURRENT FILING DATE: 1996-05-09
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Related to
; OTHER INFORMATION: human translationally controlled tumor protein
US-08-647-405B-3
```

```
Query Match          27.3%; Score 3; DB 3; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches      3; Conservative      0; Mismatches      0; Indels      0; Gaps      0;
```

```
Qy      1 ARK 3
        |||
Db      3 ARK 5
```



RESULT 33  
 US-08-647-405B-4  
 ; Sequence 4, Application US/08647405B  
 ; Patent No. 6228654  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Chait, Brian T.  
 ; APPLICANT: Zhao, Yingming  
 ; APPLICANT: Kent, Stephen B.H.  
 ; TITLE OF INVENTION: METHODS FOR STRUCTURE ANALYSIS OF OLIGOSACCHARIDES  
 ; FILE REFERENCE: Oligosaccharides  
 ; CURRENT APPLICATION NUMBER: US/08/647,405B  
 ; CURRENT FILING DATE: 1996-05-09  
 ; NUMBER OF SEQ ID NOS: 7  
 ; SOFTWARE: PatentIn Ver. 2.1  
 ; SEQ ID NO 4  
 ; LENGTH: 11  
 ; TYPE: PRT  
 ; ORGANISM: Artificial Sequence  
 ; FEATURE:  
 ; OTHER INFORMATION: Description of Artificial Sequence: Related to  
 ; OTHER INFORMATION: human translationally controlled tumor protein  
 US-08-647-405B-4

Query Match 27.3%; Score 3; DB 3; Length 11;  
 Best Local Similarity 100.0%; Pred. No. 1.8e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ARK 3  
 |||  
 Db 3 ARK 5

RESULT 34  
 US-09-177-249-212  
 ; Sequence 212, Application US/09177249  
 ; Patent No. 6229064  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Fischer, Robert L.  
 ; APPLICANT: Ohad, Nir  
 ; APPLICANT: Kiyosue, Tomohiro  
 ; APPLICANT: Yadegari, Ramin  
 ; APPLICANT: Margossian, Linda  
 ; APPLICANT: Harada, John  
 ; APPLICANT: Goldberg, Robert B.  
 ; APPLICANT: The Regents of the University of California  
 ; TITLE OF INVENTION: Nucleic Acids That Control Seed and Fruit  
 ; TITLE OF INVENTION: Development in Plants  
 ; FILE REFERENCE: 023070-086120US  
 ; CURRENT APPLICATION NUMBER: US/09/177,249  
 ; CURRENT FILING DATE: 1998-10-22  
 ; EARLIER APPLICATION NUMBER: US 09/071,838  
 ; EARLIER FILING DATE: 1998-05-01  
 ; NUMBER OF SEQ ID NOS: 324  
 ; SOFTWARE: PatentIn Ver. 2.0  
 ; SEQ ID NO 212  
 ; LENGTH: 11  
 ; TYPE: PRT

; ORGANISM: Arabidopsis sp.  
US-09-177-249-212

Query Match 27.3%; Score 3; DB 3; Length 11;  
Best Local Similarity 100.0%; Pred. No. 1.8e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 RKS 4  
|||  
Db 2 RKS 4

RESULT 35

US-09-248-588-70

; Sequence 70, Application US/09248588  
; Patent No. 6231864  
; GENERAL INFORMATION:  
; APPLICANT: Birkett, Ashley J.  
; TITLE OF INVENTION: Strategically Modified Hepatitis B Core Proteins and  
; TITLE OF INVENTION: their Derivatives  
; FILE REFERENCE: SYN-101 4564/69529  
; CURRENT APPLICATION NUMBER: US/09/248,588  
; CURRENT FILING DATE: 1999-02-11  
; EARLIER APPLICATION NUMBER: 60/074537  
; EARLIER FILING DATE: 1998-02-12  
; NUMBER OF SEQ ID NOS: 113  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 70  
; LENGTH: 11  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
US-09-248-588-70

Query Match 27.3%; Score 3; DB 3; Length 11;  
Best Local Similarity 100.0%; Pred. No. 1.8e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 SRD 6  
|||  
Db 8 SRD 10

RESULT 36

US-08-160-604-73

; Sequence 73, Application US/08160604  
; Patent No. 6232522  
; GENERAL INFORMATION:  
; APPLICANT: Harley, John  
; APPLICANT: James, Judith A.  
; APPLICANT: Scofield, R. H.  
; TITLE OF INVENTION: PEPTIDE INDUCTION OF AUTOIMMUNITY AND CLINICAL  
SYMPTOMATOLOGY  
; NUMBER OF SEQUENCES: 127  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Patrea L. Pabst  
; STREET: 1100 Peachtree Street, Suite 2800  
; CITY: Atlanta

```

; STATE: Georgia
; COUNTRY: USA
; ZIP: 30309-4530
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/160,604
; FILING DATE: 30-NOV-1993
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/867,819
; FILING DATE: 13-APR-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/648,205
; FILING DATE: 31-JAN-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/472,947
; FILING DATE: 31-JAN-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Pabst, Patrea L.
; REGISTRATION NUMBER: 31,284
; REFERENCE/DOCKET NUMBER: OMRf114CIP(3)
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (404)-815-6508
; TELEFAX: (404)-815-6555
; INFORMATION FOR SEQ ID NO: 73:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE: N-terminal
US-08-160-604-73

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```

Query Match          27.3%; Score 3; DB 3; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches      3; Conservative      0; Mismatches      0; Indels      0; Gaps      0;

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```

Qy      7 MTA 9
      |||
Db      9 MTA 11

```

```

RESULT 37
US-09-410-025-1
; Sequence 1, Application US/09410025
; Patent No. 6251623
; GENERAL INFORMATION:
; APPLICANT: ARAHIRA, MASAOMI
; APPLICANT: FUKAZAWA, CHIKAFUSA

```

; TITLE OF INVENTION: QUICK ASSAY METHOD FOR THE ACTIVITY OF A PLANT-DERIVED,  
ASPARAGINE  
; TITLE OF INVENTION: RESIDUE-SPECIFIC ENDOPROTEASE  
; FILE REFERENCE: 8361-0008-0  
; CURRENT APPLICATION NUMBER: US/09/410,025  
; CURRENT FILING DATE: 1999-10-01  
; PRIOR APPLICATION NUMBER: JP10-327536  
; PRIOR FILING DATE: 1998-11-04  
; NUMBER OF SEQ ID NOS: 11  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 1  
; LENGTH: 11  
; TYPE: PRT  
; ORGANISM: Glycine max  
US-09-410-025-1

Query Match 27.3%; Score 3; DB 3; Length 11;  
Best Local Similarity 100.0%; Pred. No. 1.8e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 KSR 5  
|||  
Db 2 KSR 4

RESULT 38

US-09-410-025-2

; Sequence 2, Application US/09410025  
; Patent No. 6251623  
; GENERAL INFORMATION:  
; APPLICANT: ARAHIRA, MASAOMI  
; APPLICANT: FUKAZAWA, CHIKAFUSA  
; TITLE OF INVENTION: QUICK ASSAY METHOD FOR THE ACTIVITY OF A PLANT-DERIVED,  
ASPARAGINE  
; TITLE OF INVENTION: RESIDUE-SPECIFIC ENDOPROTEASE  
; FILE REFERENCE: 8361-0008-0  
; CURRENT APPLICATION NUMBER: US/09/410,025  
; CURRENT FILING DATE: 1999-10-01  
; PRIOR APPLICATION NUMBER: JP10-327536  
; PRIOR FILING DATE: 1998-11-04  
; NUMBER OF SEQ ID NOS: 11  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 2  
; LENGTH: 11  
; TYPE: PRT  
; ORGANISM: Glycine max  
US-09-410-025-2

Query Match 27.3%; Score 3; DB 3; Length 11;  
Best Local Similarity 100.0%; Pred. No. 1.8e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 KSR 5  
|||  
Db 2 KSR 4

RESULT 39

US-09-410-025-3

```
; Sequence 3, Application US/09410025
; Patent No. 6251623
; GENERAL INFORMATION:
; APPLICANT: ARAHIRA, MASAOMI
; APPLICANT: FUKAZAWA, CHIKAFUSA
; TITLE OF INVENTION: QUICK ASSAY METHOD FOR THE ACTIVITY OF A PLANT-DERIVED,
ASPARAGINE
; TITLE OF INVENTION: RESIDUE-SPECIFIC ENDOPROTEASE
; FILE REFERENCE: 8361-0008-0
; CURRENT APPLICATION NUMBER: US/09/410,025
; CURRENT FILING DATE: 1999-10-01
; PRIOR APPLICATION NUMBER: JP10-327536
; PRIOR FILING DATE: 1998-11-04
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 3
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Glycine max
US-09-410-025-3
```

```
Query Match          27.3%; Score 3; DB 3; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches      3; Conservative      0; Mismatches      0; Indels      0; Gaps      0;
```

```
Qy      3 KSR 5
        |||
Db      2 KSR 4
```

RESULT 40

US-09-410-025-4

```
; Sequence 4, Application US/09410025
; Patent No. 6251623
; GENERAL INFORMATION:
; APPLICANT: ARAHIRA, MASAOMI
; APPLICANT: FUKAZAWA, CHIKAFUSA
; TITLE OF INVENTION: QUICK ASSAY METHOD FOR THE ACTIVITY OF A PLANT-DERIVED,
ASPARAGINE
; TITLE OF INVENTION: RESIDUE-SPECIFIC ENDOPROTEASE
; FILE REFERENCE: 8361-0008-0
; CURRENT APPLICATION NUMBER: US/09/410,025
; CURRENT FILING DATE: 1999-10-01
; PRIOR APPLICATION NUMBER: JP10-327536
; PRIOR FILING DATE: 1998-11-04
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 4
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Glycine max
US-09-410-025-4
```

```
Query Match          27.3%; Score 3; DB 3; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
```

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 KSR 5  
|||  
Db 2 KSR 4

RESULT 41

US-09-410-025-5

; Sequence 5, Application US/09410025

; Patent No. 6251623

; GENERAL INFORMATION:

; APPLICANT: ARAHIRA, MASAOMI

; APPLICANT: FUKAZAWA, CHIKAFUSA

; TITLE OF INVENTION: QUICK ASSAY METHOD FOR THE ACTIVITY OF A PLANT-DERIVED, ASPARAGINE

; TITLE OF INVENTION: RESIDUE-SPECIFIC ENDOPROTEASE

; FILE REFERENCE: 8361-0008-0

; CURRENT APPLICATION NUMBER: US/09/410,025

; CURRENT FILING DATE: 1999-10-01

; PRIOR APPLICATION NUMBER: JP10-327536

; PRIOR FILING DATE: 1998-11-04

; NUMBER OF SEQ ID NOS: 11

; SOFTWARE: PatentIn version 3.0

; SEQ ID NO 5

; LENGTH: 11

; TYPE: PRT

; ORGANISM: Glycine max

US-09-410-025-5

Query Match 27.3%; Score 3; DB 3; Length 11;

Best Local Similarity 100.0%; Pred. No. 1.8e+03;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 KSR 5  
|||  
Db 2 KSR 4

RESULT 42

US-09-410-025-6

; Sequence 6, Application US/09410025

; Patent No. 6251623

; GENERAL INFORMATION:

; APPLICANT: ARAHIRA, MASAOMI

; APPLICANT: FUKAZAWA, CHIKAFUSA

; TITLE OF INVENTION: QUICK ASSAY METHOD FOR THE ACTIVITY OF A PLANT-DERIVED, ASPARAGINE

; TITLE OF INVENTION: RESIDUE-SPECIFIC ENDOPROTEASE

; FILE REFERENCE: 8361-0008-0

; CURRENT APPLICATION NUMBER: US/09/410,025

; CURRENT FILING DATE: 1999-10-01

; PRIOR APPLICATION NUMBER: JP10-327536

; PRIOR FILING DATE: 1998-11-04

; NUMBER OF SEQ ID NOS: 11

; SOFTWARE: PatentIn version 3.0

; SEQ ID NO 6

; LENGTH: 11  
; TYPE: PRT  
; ORGANISM: Glycine max  
US-09-410-025-6

Query Match 27.3%; Score 3; DB 3; Length 11;  
Best Local Similarity 100.0%; Pred. No. 1.8e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 KSR 5  
|||  
Db 2 KSR 4

RESULT 43

US-09-410-025-7

; Sequence 7, Application US/09410025

; Patent No. 6251623

; GENERAL INFORMATION:

; APPLICANT: ARAHIRA, MASAOMI

; APPLICANT: FUKAZAWA, CHIKAFUSA

; TITLE OF INVENTION: QUICK ASSAY METHOD FOR THE ACTIVITY OF A PLANT-DERIVED,  
ASPARAGINE

; TITLE OF INVENTION: RESIDUE-SPECIFIC ENDOPROTEASE

; FILE REFERENCE: 8361-0008-0

; CURRENT APPLICATION NUMBER: US/09/410,025

; CURRENT FILING DATE: 1999-10-01

; PRIOR APPLICATION NUMBER: JP10-327536

; PRIOR FILING DATE: 1998-11-04

; NUMBER OF SEQ ID NOS: 11

; SOFTWARE: PatentIn version 3.0

; SEQ ID NO 7

; LENGTH: 11

; TYPE: PRT

; ORGANISM: Glycine max

US-09-410-025-7

Query Match 27.3%; Score 3; DB 3; Length 11;  
Best Local Similarity 100.0%; Pred. No. 1.8e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 KSR 5  
|||  
Db 2 KSR 4

RESULT 44

US-09-410-025-8

; Sequence 8, Application US/09410025

; Patent No. 6251623

; GENERAL INFORMATION:

; APPLICANT: ARAHIRA, MASAOMI

; APPLICANT: FUKAZAWA, CHIKAFUSA

; TITLE OF INVENTION: QUICK ASSAY METHOD FOR THE ACTIVITY OF A PLANT-DERIVED,  
ASPARAGINE

; TITLE OF INVENTION: RESIDUE-SPECIFIC ENDOPROTEASE

; FILE REFERENCE: 8361-0008-0

; CURRENT APPLICATION NUMBER: US/09/410,025  
; CURRENT FILING DATE: 1999-10-01  
; PRIOR APPLICATION NUMBER: JP10-327536  
; PRIOR FILING DATE: 1998-11-04  
; NUMBER OF SEQ ID NOS: 11  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 8  
; LENGTH: 11  
; TYPE: PRT  
; ORGANISM: Glycine max  
US-09-410-025-8

Query Match 27.3%; Score 3; DB 3; Length 11;  
Best Local Similarity 100.0%; Pred. No. 1.8e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 KSR 5  
|||  
Db 2 KSR 4

RESULT 45

US-09-410-025-9

; Sequence 9, Application US/09410025  
; Patent No. 6251623  
; GENERAL INFORMATION:  
; APPLICANT: ARAHIRA, MASAOMI  
; APPLICANT: FUKAZAWA, CHIKAFUSA  
; TITLE OF INVENTION: QUICK ASSAY METHOD FOR THE ACTIVITY OF A PLANT-DERIVED,  
ASPARAGINE  
; TITLE OF INVENTION: RESIDUE-SPECIFIC ENDOPROTEASE  
; FILE REFERENCE: 8361-0008-0  
; CURRENT APPLICATION NUMBER: US/09/410,025  
; CURRENT FILING DATE: 1999-10-01  
; PRIOR APPLICATION NUMBER: JP10-327536  
; PRIOR FILING DATE: 1998-11-04  
; NUMBER OF SEQ ID NOS: 11  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 9  
; LENGTH: 11  
; TYPE: PRT  
; ORGANISM: Glycine max  
US-09-410-025-9

Query Match 27.3%; Score 3; DB 3; Length 11;  
Best Local Similarity 100.0%; Pred. No. 1.8e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 KSR 5  
|||  
Db 2 KSR 4

RESULT 46

US-09-410-025-10

; Sequence 10, Application US/09410025  
; Patent No. 6251623



; GENERAL INFORMATION:  
; APPLICANT: ARAHIRA, MASAOMI  
; APPLICANT: FUKAZAWA, CHIKAFUSA  
; TITLE OF INVENTION: QUICK ASSAY METHOD FOR THE ACTIVITY OF A PLANT-DERIVED,  
ASPARAGINE  
; TITLE OF INVENTION: RESIDUE-SPECIFIC ENDOPROTEASE  
; FILE REFERENCE: 8361-0008-0  
; CURRENT APPLICATION NUMBER: US/09/410,025  
; CURRENT FILING DATE: 1999-10-01  
; PRIOR APPLICATION NUMBER: JP10-327536  
; PRIOR FILING DATE: 1998-11-04  
; NUMBER OF SEQ ID NOS: 11  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 10  
; LENGTH: 11  
; TYPE: PRT  
; ORGANISM: Glycine max  
US-09-410-025-10

Query Match 27.3%; Score 3; DB 3; Length 11;  
Best Local Similarity 100.0%; Pred. No. 1.8e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 KSR 5  
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Db 2 KSR 4

#### RESULT 47

US-09-025-769B-186

; Sequence 186, Application US/09025769B

; Patent No. 6300064

; GENERAL INFORMATION:

; APPLICANT: Knappik, Achim

; APPLICANT: Pack, Peter

; APPLICANT: Ilag, Vic

; APPLICANT: Ge, Liming

; APPLICANT: Moroney, Simon

; APPLICANT: Plueckthun, Andreas

; TITLE OF INVENTION: Protein/(Poly)peptide libraries

; NUMBER OF SEQUENCES: 373

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave

; STREET: 1251 Avenue of the Americas

; CITY: New York

; STATE: New York

; COUNTRY: USA

; ZIP: 10021

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/025,769B

; FILING DATE: 18-FEB-1998

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: EP 95 11 3021.0  
 ; FILING DATE: 18-AUG-1995  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: James F. Haley, Jr., Esq.  
 ; REGISTRATION NUMBER: 27,794  
 ; REFERENCE/DOCKET NUMBER: MORPHO/5  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: (212)596-9000  
 ; TELEFAX: (212)596-9090  
 ; INFORMATION FOR SEQ ID NO: 186:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 11 amino acids  
 ; TYPE: amino acid  
 ; STRANDEDNESS:  
 ; TOPOLOGY: linear  
 ; MOLECULE TYPE: protein  
 ; FRAGMENT TYPE: internal  
 US-09-025-769B-186

Query Match 27.3%; Score 3; DB 4; Length 11;  
 Best Local Similarity 100.0%; Pred. No. 1.8e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 TAI 10  
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 Db 4 TAI 6

RESULT 48

US-09-227-357-567

; Sequence 567, Application US/09227357  
 ; Patent No. 6342581  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Fischer et al.  
 ; TITLE OF INVENTION: 123 Human Secreted Proteins  
 ; FILE REFERENCE: PZ010P1  
 ; CURRENT APPLICATION NUMBER: US/09/227,357  
 ; CURRENT FILING DATE: 1999-01-08  
 ; EARLIER APPLICATION NUMBER: PCT/US98/13684  
 ; EARLIER FILING DATE: 1998-07-07  
 ; EARLIER APPLICATION NUMBER: 60/051,926  
 ; EARLIER FILING DATE: 1997-07-08  
 ; EARLIER APPLICATION NUMBER: 60/052,793  
 ; EARLIER FILING DATE: 1997-07-08  
 ; EARLIER APPLICATION NUMBER: 60/051,925  
 ; EARLIER FILING DATE: 1997-07-08  
 ; EARLIER APPLICATION NUMBER: 60/051,929  
 ; EARLIER FILING DATE: 1997-07-08  
 ; EARLIER APPLICATION NUMBER: 60/052,803  
 ; EARLIER FILING DATE: 1997-07-08  
 ; EARLIER APPLICATION NUMBER: 60/052,732  
 ; EARLIER FILING DATE: 1997-07-08  
 ; EARLIER APPLICATION NUMBER: 60/051,931  
 ; EARLIER FILING DATE: 1997-07-08  
 ; EARLIER APPLICATION NUMBER: 60/051,932  
 ; EARLIER FILING DATE: 1997-07-08  
 ; EARLIER APPLICATION NUMBER: 60/051,916

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; EARLIER FILING DATE: 1997-07-08
; EARLIER APPLICATION NUMBER: 60/051,930
; EARLIER FILING DATE: 1997-07-08
; EARLIER APPLICATION NUMBER: 60/051,918
; EARLIER FILING DATE: 1997-07-08
; EARLIER APPLICATION NUMBER: 60/051,920
; EARLIER FILING DATE: 1997-07-08
; EARLIER APPLICATION NUMBER: 60/052,733
; EARLIER FILING DATE: 1997-07-08
; EARLIER APPLICATION NUMBER: 60/052,795
; EARLIER FILING DATE: 1997-07-08
; EARLIER APPLICATION NUMBER: 60/051,919
; EARLIER FILING DATE: 1997-07-08
; EARLIER APPLICATION NUMBER: 60/051,928
; EARLIER FILING DATE: 1997-07-08
; EARLIER APPLICATION NUMBER: 60/055,722
; EARLIER FILING DATE: 1997-08-18
; EARLIER APPLICATION NUMBER: 60/055,723
; EARLIER FILING DATE: 1997-08-18
; EARLIER APPLICATION NUMBER: 60/055,948
; EARLIER FILING DATE: 1997-08-18
; EARLIER APPLICATION NUMBER: 60/055,949
; EARLIER FILING DATE: 1997-08-18
; EARLIER APPLICATION NUMBER: 60/055,953
; EARLIER FILING DATE: 1997-08-18
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; EARLIER FILING DATE: 1997-08-18
; EARLIER APPLICATION NUMBER: 60/055,947
; EARLIER FILING DATE: 1997-08-18
; EARLIER APPLICATION NUMBER: 60/055,964
; EARLIER FILING DATE: 1997-08-18
; EARLIER APPLICATION NUMBER: 60/056,360
; EARLIER FILING DATE: 1997-08-18
; EARLIER APPLICATION NUMBER: 60/055,684
; EARLIER FILING DATE: 1997-08-18
; EARLIER APPLICATION NUMBER: 60/055,984
; EARLIER FILING DATE: 1997-08-18
; EARLIER APPLICATION NUMBER: 60/055,954
; EARLIER FILING DATE: 1997-08-18
; EARLIER APPLICATION NUMBER: 60/058,785
; EARLIER FILING DATE: 1997-09-12
; EARLIER APPLICATION NUMBER: 60/058,664
; EARLIER FILING DATE: 1997-09-12
; EARLIER APPLICATION NUMBER: 60/058,660
; EARLIER FILING DATE: 1997-09-12
; EARLIER APPLICATION NUMBER: 60/058,661
; EARLIER FILING DATE: 1997-09-12
; NUMBER OF SEQ ID NOS: 672
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 567
;   LENGTH: 11
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-227-357-567

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Query Match          27.3%;  Score 3;  DB 4;  Length 11;
Best Local Similarity 100.0%;  Pred. No. 1.8e+03;

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Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 AIK 11  
|||  
Db 7 AIK 9

RESULT 49

US-09-314-268-171

; Sequence 171, Application US/09314268  
; Patent No. 6346377  
; GENERAL INFORMATION:  
; APPLICANT: Doorbar, John  
; TITLE OF INVENTION: IMPROVEMENTS IN OR RELATING TO SCREENING FOR PAPILLOMA  
; TITLE OF INVENTION: VIRUSES  
; FILE REFERENCE: 3789/80902  
; CURRENT APPLICATION NUMBER: US/09/314,268  
; CURRENT FILING DATE: 1999-03-19  
; EARLIER APPLICATION NUMBER: 09/314,268  
; EARLIER FILING DATE: 1999-05-18  
; NUMBER OF SEQ ID NOS: 179  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 171  
; LENGTH: 11  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
; OTHER INFORMATION: Peptide

US-09-314-268-171

Query Match 27.3%; Score 3; DB 4; Length 11;  
Best Local Similarity 100.0%; Pred. No. 1.8e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 SRD 6  
|||  
Db 2 SRD 4

RESULT 50

US-09-277-599B-2

; Sequence 2, Application US/09277599B  
; Patent No. 6395879  
; GENERAL INFORMATION:  
; APPLICANT: Mandrell, David  
; APPLICANT: Bates, Anna  
; APPLICANT: Brandon, David  
; TITLE OF INVENTION: Monoclonal Antibodies Against Campylobacter jejuni and  
Campylobacter coli  
; TITLE OF INVENTION: Outer Membrane Antigens  
; FILE REFERENCE: Mandrell  
; CURRENT APPLICATION NUMBER: US/09/277,599B  
; CURRENT FILING DATE: 1999-03-26  
; PRIOR APPLICATION NUMBER: US 60/080,166  
; PRIOR FILING DATE: 1998-03-31  
; NUMBER OF SEQ ID NOS: 2

; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 2  
; LENGTH: 11  
; TYPE: PRT  
; ORGANISM: Campylobacter jejuni  
; FEATURE:  
; NAME/KEY: misc\_feature  
; LOCATION: ()..()  
; OTHER INFORMATION: The undetermined amino acid may or may not exist  
US-09-277-599B-2

Query Match 27.3%; Score 3; DB 4; Length 11;  
Best Local Similarity 100.0%; Pred. No. 1.8e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 AIK 11  
|||  
Db 7 AIK 9

# RESULT 51

US-09-149-476-698

; Sequence 698, Application US/09149476  
; Patent No. 6420526  
; GENERAL INFORMATION:  
; APPLICANT: Rosen et al.  
; TITLE OF INVENTION: 186.Human Secreted proteins  
; FILE REFERENCE: PZ002P1  
; CURRENT APPLICATION NUMBER: US/09/149,476  
; CURRENT FILING DATE: 1998-09-08  
; EARLIER APPLICATION NUMBER: PCT/US98/04493  
; EARLIER FILING DATE: 1998-03-06  
; EARLIER APPLICATION NUMBER: 60/040,162  
; EARLIER FILING DATE: 1997-03-07  
; EARLIER APPLICATION NUMBER: 60/040,333  
; EARLIER FILING DATE: 1997-03-07  
; EARLIER APPLICATION NUMBER: 60/038,621  
; EARLIER FILING DATE: 1997-03-07  
; EARLIER APPLICATION NUMBER: 60/040,626  
; EARLIER FILING DATE: 1997-03-07  
; EARLIER APPLICATION NUMBER: 60/040,334  
; EARLIER FILING DATE: 1997-03-07  
; EARLIER APPLICATION NUMBER: 60/040,336  
; EARLIER FILING DATE: 1997-03-07  
; EARLIER APPLICATION NUMBER: 60/040,163  
; EARLIER FILING DATE: 1997-03-07  
; EARLIER APPLICATION NUMBER: 60/047,600  
; EARLIER FILING DATE: 1997-05-23  
; EARLIER APPLICATION NUMBER: 60/047,615  
; EARLIER FILING DATE: 1997-05-23  
; EARLIER APPLICATION NUMBER: 60/047,597  
; EARLIER FILING DATE: 1997-05-23  
; EARLIER APPLICATION NUMBER: 60/047,502  
; EARLIER FILING DATE: 1997-05-23  
; EARLIER APPLICATION NUMBER: 60/047,633  
; EARLIER FILING DATE: 1997-05-23  
; EARLIER APPLICATION NUMBER: 60/047,583

; EARLIER FILING DATE: 1997-05-23  
; EARLIER APPLICATION NUMBER: 60/047,617  
; EARLIER FILING DATE: 1997-05-23  
; EARLIER APPLICATION NUMBER: 60/047,618  
; EARLIER FILING DATE: 1997-05-23  
; EARLIER APPLICATION NUMBER: 60/047,503  
; EARLIER FILING DATE: 1997-05-23  
; EARLIER APPLICATION NUMBER: 60/047,592  
; EARLIER FILING DATE: 1997-05-23  
; EARLIER APPLICATION NUMBER: 60/047,581  
; EARLIER FILING DATE: 1997-05-23  
; EARLIER APPLICATION NUMBER: 60/047,584  
; EARLIER FILING DATE: 1997-05-23  
; EARLIER APPLICATION NUMBER: 60/047,500  
; EARLIER FILING DATE: 1997-05-23  
; EARLIER APPLICATION NUMBER: 60/047,587  
; EARLIER FILING DATE: 1997-05-23  
; EARLIER APPLICATION NUMBER: 60/047,492  
; EARLIER FILING DATE: 1997-05-23  
; EARLIER APPLICATION NUMBER: 60/047,598  
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; EARLIER APPLICATION NUMBER: 60/047,613  
; EARLIER FILING DATE: 1997-05-23  
; EARLIER APPLICATION NUMBER: 60/047,582  
; EARLIER FILING DATE: 1997-05-23  
; EARLIER APPLICATION NUMBER: 60/047,596  
; EARLIER FILING DATE: 1997-05-23  
; EARLIER APPLICATION NUMBER: 60/047,612  
; EARLIER FILING DATE: 1997-05-23  
; EARLIER APPLICATION NUMBER: 60/047,632  
; EARLIER FILING DATE: 1997-05-23  
; EARLIER APPLICATION NUMBER: 60/047,601  
; EARLIER FILING DATE: 1997-05-23  
; EARLIER APPLICATION NUMBER: 60/043,580  
; EARLIER FILING DATE: 1997-04-11  
; EARLIER APPLICATION NUMBER: 60/043,568  
; EARLIER FILING DATE: 1997-04-11  
; EARLIER APPLICATION NUMBER: 60/043,314  
; EARLIER FILING DATE: 1997-04-11  
; EARLIER APPLICATION NUMBER: 60/043,569  
; EARLIER FILING DATE: 1997-04-11  
; EARLIER APPLICATION NUMBER: 60/043,311  
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; EARLIER APPLICATION NUMBER: 60/043,671  
; EARLIER FILING DATE: 1997-04-11  
; EARLIER APPLICATION NUMBER: 60/043,674  
; EARLIER FILING DATE: 1997-04-11  
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; EARLIER APPLICATION NUMBER: 60/043,312  
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; EARLIER APPLICATION NUMBER: 60/043,313  
; EARLIER FILING DATE: 1997-04-11  
; EARLIER APPLICATION NUMBER: 60/043,672  
; EARLIER FILING DATE: 1997-04-11  
; EARLIER APPLICATION NUMBER: 60/043,315  
; EARLIER FILING DATE: 1997-04-11

; EARLIER APPLICATION NUMBER: 60/048,974  
; EARLIER FILING DATE: 1997-06-06  
; EARLIER APPLICATION NUMBER: 60/056,886  
; EARLIER FILING DATE: 1997-08-22  
; EARLIER APPLICATION NUMBER: 60/056,877  
; EARLIER FILING DATE: 1997-08-22  
; EARLIER APPLICATION NUMBER: 60/056,889  
; EARLIER FILING DATE: 1997-08-22  
; EARLIER APPLICATION NUMBER: 60/056,893  
; EARLIER FILING DATE: 1997-08-22  
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; EARLIER APPLICATION NUMBER: 60/056,878  
; EARLIER FILING DATE: 1997-08-22  
; EARLIER APPLICATION NUMBER: 60/056,662  
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; EARLIER APPLICATION NUMBER: 60/056,872  
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; EARLIER APPLICATION NUMBER: 60/056,882  
; EARLIER FILING DATE: 1997-08-22  
; EARLIER APPLICATION NUMBER: 60/056,637  
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; EARLIER APPLICATION NUMBER: 60/056,903  
; EARLIER FILING DATE: 1997-08-22  
; EARLIER APPLICATION NUMBER: 60/056,888  
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; EARLIER APPLICATION NUMBER: 60/056,880  
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; EARLIER APPLICATION NUMBER: 60/056,894  
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; EARLIER APPLICATION NUMBER: 60/056,911  
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; EARLIER APPLICATION NUMBER: 60/056,636  
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; EARLIER APPLICATION NUMBER: 60/056,874  
; EARLIER FILING DATE: 1997-08-22  
; EARLIER APPLICATION NUMBER: 60/056,910  
; EARLIER FILING DATE: 1997-08-22  
; EARLIER APPLICATION NUMBER: 60/056,864  
; EARLIER FILING DATE: 1997-08-22  
; EARLIER APPLICATION NUMBER: 60/056,631  
; EARLIER FILING DATE: 1997-08-22  
; EARLIER APPLICATION NUMBER: 60/056,845  
; EARLIER FILING DATE: 1997-08-22  
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; EARLIER APPLICATION NUMBER: 60/057,761  
; EARLIER FILING DATE: 1997-08-22  
; EARLIER APPLICATION NUMBER: 60/047,595  
; EARLIER FILING DATE: 1997-05-23  
; EARLIER APPLICATION NUMBER: 60/047,599  
; EARLIER FILING DATE: 1997-05-23  
; EARLIER APPLICATION NUMBER: 60/047,588  
; EARLIER FILING DATE: 1997-05-23  
; EARLIER APPLICATION NUMBER: 60/047,585

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; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,586
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,590
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,594
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,589
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; EARLIER APPLICATION NUMBER: 60/047,593
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,614
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/043,578
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/043,576
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/047,501
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/043,670
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/056,632
; EARLIER FILING DATE: 1997-08-22
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; EARLIER APPLICATION NUMBER: 60/056,876
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,881
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,909
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,875
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,862
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,887
; EARLIER FILING DATE: 1997-08-22
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; EARLIER APPLICATION NUMBER: 60/048,964
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/057,650
; EARLIER FILING DATE: 1997-09-05
; EARLIER APPLICATION NUMBER: 60/056,884
; EARLIER FILING DATE: 1997-08-22
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; EARLIER FILING DATE: 1997-09-05
; EARLIER APPLICATION NUMBER: 60/049,610
; EARLIER FILING DATE: 1997-06-13
; EARLIER APPLICATION NUMBER: 60/061,060
; EARLIER FILING DATE: 1997-10-02

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Query Match          27.3%;  Score 3;  DB 4;  Length 11;
Best Local Similarity 100.0%;  Pred. No. 1.8e+03;
Matches      3;  Conservative    0;  Mismatches    0;  Indels      0;  Gaps      0;

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Qy 9 AIK 11



Db                    |||  
                      4 AIK 6

RESULT 52

US-09-177-165A-1

; Sequence 1, Application US/09177165A  
; Patent No. 6426205  
; GENERAL INFORMATION:  
; APPLICANT: Tyers, Mike  
; APPLICANT: Willems, Andrew  
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR MODULATING UBIQUITIN  
; TITLE OF INVENTION: DEPENDENT PROTEOLYSIS  
; FILE REFERENCE: 11757.10USU1  
; CURRENT APPLICATION NUMBER: US/09/177,165A  
; CURRENT FILING DATE: 1998-10-22  
; PRIOR APPLICATION NUMBER: 60/092,443  
; PRIOR FILING DATE: 1998-07-10  
; PRIOR APPLICATION NUMBER: 60/063,254  
; PRIOR FILING DATE: 1997-10-24  
; NUMBER OF SEQ ID NOS: 50  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 1  
; LENGTH: 11  
; TYPE: PRT  
; ORGANISM: Saccharomyces cerevisiae  
US-09-177-165A-1

Query Match                    27.3%; Score 3; DB 4; Length 11;  
Best Local Similarity       100.0%; Pred. No. 1.8e+03;  
Matches       3; Conservative       0; Mismatches       0; Indels       0; Gaps       0;

Qy                    8 TAI 10  
                      |||  
Db                    4 TAI 6

RESULT 53

US-08-255-208A-77

; Sequence 77, Application US/08255208A  
; Patent No. 6440656  
; GENERAL INFORMATION:  
; APPLICANT: Bolognesi, Dani P.  
; APPLICANT: Matthews, Thomas J.  
; APPLICANT: Wild, Carl T.  
; APPLICANT: Barney, Shawn O.  
; APPLICANT: Lambert, Dennis M.  
; APPLICANT: Petteway Jr., Stephen R.  
; TITLE OF INVENTION: SYNTHETIC PEPTIDE INHIBITORS OF HIV  
; TITLE OF INVENTION: TRANSMISSION  
; NUMBER OF SEQUENCES: 111  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Pennie & Edmonds LLP  
; STREET: 1155 Avenue of the Americas  
; CITY: New York  
; STATE: New York  
; COUNTRY: USA

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; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/255,208A
; FILING DATE: 07-JUN-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Coruzzi, Laura A.
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 7872-010
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 77:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 1
; OTHER INFORMATION: /label= A
; OTHER INFORMATION: /note= "Preceeding this amino acid, there may be an
amino group
; OTHER INFORMATION: an acetyl group, a 9-fluorenylmethoxy-carbonyl group,
a hydroph
; OTHER INFORMATION: group or a macromolecular carrier group."
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 11
; OTHER INFORMATION: /label= B
; OTHER INFORMATION: /note= "Following this amino acid, there may be a
carboxyl grou
; OTHER INFORMATION: an amido group, a hydrophobic group, or a
macromolecular carrie
; OTHER INFORMATION: group."
US-08-255-208A-77

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Query Match          27.3%; Score 3; DB 4; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches      3; Conservative    0; Mismatches    0; Indels      0; Gaps      0;

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Qy      2 RKS 4
      |||
Db      5 RKS 7

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RESULT 54
US-08-469-260A-550
; Sequence 550, Application US/08469260A

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; Patent No. 6451578
; GENERAL INFORMATION:
;   APPLICANT: JOHN N. SIMONS
;   APPLICANT: TAMI J. PILOT-MATIAS
;   APPLICANT: GEORGE J. DAWSON
;   APPLICANT: GEORGE G. SCHLAUDER
;   APPLICANT: SURESH M. DESAI
;   APPLICANT: THOMAS P. LEARY
;   APPLICANT: ANTHONY SCOTT MUEHROFF
;   APPLICANT: JAMES C. ERKER
;   APPLICANT: SHERI L. BUIJK
;   APPLICANT: ISA K. MUSHAHWAR
;   TITLE OF INVENTION: NON-A, NON-B, NON-C, NON-D, NON-E HEPATITIS
;   TITLE OF INVENTION: REAGENTS AND METHODS FOR THEIR USE
;   NUMBER OF SEQUENCES: 716
;   CORRESPONDENCE ADDRESS:
;     ADDRESSEE: ABBOTT LABORATORIES D377/AP6D
;     STREET: 100 ABBOTT PARK ROAD
;     CITY: ABBOTT PARK
;     STATE: IL
;     COUNTRY: USA
;     ZIP: 60064-3500
;   COMPUTER READABLE FORM:
;     MEDIUM TYPE: Floppy disk
;     COMPUTER: IBM PC compatible
;     OPERATING SYSTEM: PC-DOS/MS-DOS
;     SOFTWARE: PatentIn Release #1.0, Version #1.25
;   CURRENT APPLICATION DATA:
;     APPLICATION NUMBER: US/08/469,260A
;     FILING DATE:
;     CLASSIFICATION:
;   PRIOR APPLICATION DATA:
;     APPLICATION NUMBER: US/08/424,550
;     FILING DATE:
;   ATTORNEY/AGENT INFORMATION:
;     NAME: POREMBSKI, PRISCILLA E.
;     REGISTRATION NUMBER: 33,207
;     REFERENCE/DOCKET NUMBER: 5527.PC.01
;   TELECOMMUNICATION INFORMATION:
;     TELEPHONE: 708-937-6365
;     TELEFAX: 708-938-2623
;   INFORMATION FOR SEQ ID NO: 550:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH: 11 amino acids
;       TYPE: amino acid
;       TOPOLOGY: linear
;     MOLECULE TYPE: protein
US-08-469-260A-550

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Query Match          27.3%; Score 3; DB 4; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches      3; Conservative      0; Mismatches      0; Indels      0; Gaps      0;

```

```

Qy      9 AIK 11
        |||
Db      2 AIK 4

```

RESULT 55

US-09-561-490E-56

; Sequence 56, Application US/09561490E

; Patent No. 6468537

; GENERAL INFORMATION:

; APPLICANT: DATTA, Syamal K

; APPLICANT: KALIYAPERUMAL, Arunan

; TITLE OF INVENTION: LOCALIZATION OF MAJOR PEPTIDE AUTOEPITOPES FOR NUCLEOSOME SPECIF

; TITLE OF INVENTION: IC T CELLS OF SYSTEMIC LUPUS ERYTHEMATOSUS

; FILE REFERENCE: 290-13U1 (53662-5017

; CURRENT APPLICATION NUMBER: US/09/561,490E

; CURRENT FILING DATE: 2000-04-28

; PRIOR APPLICATION NUMBER: US 60/131,448

; PRIOR FILING DATE: 1999-04-28

; NUMBER OF SEQ ID NOS: 61

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 56

; LENGTH: 11

; TYPE: PRT

; ORGANISM: Artificial sequence

; FEATURE:

; OTHER INFORMATION: Histone fragment

US-09-561-490E-56

Query Match 27.3%; Score 3; DB 4; Length 11;

Best Local Similarity 100.0%; Pred. No. 1.8e+03;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 KSR 5

|||

Db 9 KSR 11

RESULT 56

US-09-104-337A-340

; Sequence 340, Application US/09104337A

; Patent No. 6492160

; GENERAL INFORMATION:

; APPLICANT: Winter, Gregory Paul

; Griffiths, Andrew David

; Williams, Samuel Cameron

; Waterhouse, Peter

; Nissim, Ahuva

; Johnson, Kevin Stuart

; Smith, Andrew John Hammond

; TITLE OF INVENTION: Methods for producing members of specific binding pairs

; NUMBER OF SEQUENCES: 600

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Audrey L. Bartnicki

; STREET: Marshall, Gerstein & Borun

; 6300 Sears Tower, 233 South Wacker Drive

; CITY: Chicago

; STATE: Illinois

; COUNTRY: USA

```

;      ZIP: 60606-6402
;
;      COMPUTER READABLE FORM:
;
;      MEDIUM TYPE: Floppy disk
;
;      COMPUTER: IBM PC compatible
;
;      OPERATING SYSTEM: PC-DOS/MS-DOS
;
;      SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
;
;      CURRENT APPLICATION DATA:
;
;      APPLICATION NUMBER: US/09/104,337A
;
;      FILING DATE: 25-Jun-1998
;
;      PRIOR APPLICATION DATA:
;
;      APPLICATION NUMBER: US 08/350,260
;
;      FILING DATE: 05-DEC-1994
;
;      APPLICATION NUMBER: GB 9110549.4
;
;      FILING DATE: 15-MAY-1991
;
;      APPLICATION NUMBER: GB 9206318.9
;
;      FILING DATE: 24-MAR-1992
;
;      APPLICATION NUMBER: PCT/GB92/00883
;
;      FILING DATE: 15-MAY-1992
;
;      APPLICATION NUMBER: PCT/GB93/00605
;
;      FILING DATE: 24-MAR-1993
;
;      APPLICATION NUMBER: US 08/150,002
;
;      FILING DATE: 31-MAR-1994
;
;      APPLICATION NUMBER: US 08/307,619
;
;      FILING DATE: 16-SEP-1994
;
;      ATTORNEY/AGENT INFORMATION:
;
;      NAME: Bartnicki, Audrey L.
;
;      REGISTRATION NUMBER: 40,499
;
;      REFERENCE/DOCKET NUMBER: 28111/32372A
;
;      TELECOMMUNICATION INFORMATION:
;
;      TELEPHONE: 312-474-6300
;
;      INFORMATION FOR SEQ ID NO: 340:
;
;      SEQUENCE CHARACTERISTICS:
;
;      LENGTH: 11 amino acids
;
;      TYPE: amino acid
;
;      STRANDEDNESS: single
;
;      TOPOLOGY: linear
;
;      SEQUENCE DESCRIPTION: SEQ ID NO: 340:
US-09-104-337A-340

```

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Query Match          27.3%;  Score 3;  DB 4;  Length 11;
Best Local Similarity 100.0%;  Pred. No. 1.8e+03;
Matches      3;  Conservative      0;  Mismatches      0;  Indels      0;  Gaps      0;

```

```

Qy      4 SRD 6
      |||
Db      2 SRD 4

```

```

RESULT 57
US-09-104-337A-342
; Sequence 342, Application US/09104337A
; Patent No. 6492160
;
;      GENERAL INFORMATION:
;
;      APPLICANT: Winter, Gregory Paul
;
;      Griffiths, Andrew David
;
;      Williams, Samuel Cameron
;
;      Waterhouse, Peter

```

```

;           Nissim, Ahuva
;           Johnson, Kevin Stuart
;           Smith, Andrew John Hammond
; TITLE OF INVENTION: Methods for producing members of specific
;                   binding pairs
; NUMBER OF SEQUENCES: 600
; CORRESPONDENCE ADDRESS:
;     ADDRESSEE: Audrey L. Bartnicki
;     STREET: Marshall, Gerstein & Borun
;             6300 Sears Tower, 233 South Wacker Drive
;     CITY: Chicago
;     STATE: Illinois
;     COUNTRY: USA
;     ZIP: 60606-6402
; COMPUTER READABLE FORM:
;     MEDIUM TYPE: Floppy disk
;     COMPUTER: IBM PC compatible
;     OPERATING SYSTEM: PC-DOS/MS-DOS
;     SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION DATA:
;     APPLICATION NUMBER: US/09/104,337A
;     FILING DATE: 25-Jun-1998
; PRIOR APPLICATION DATA:
;     APPLICATION NUMBER: US 08/350,260
;     FILING DATE: 05-DEC-1994
;     APPLICATION NUMBER: GB 9110549.4
;     FILING DATE: 15-MAY-1991
;     APPLICATION NUMBER: GB 9206318.9
;     FILING DATE: 24-MAR-1992
;     APPLICATION NUMBER: PCT/GB92/00883
;     FILING DATE: 15-MAY-1992
;     APPLICATION NUMBER: PCT/GB93/00605
;     FILING DATE: 24-MAR-1993
;     APPLICATION NUMBER: US 08/150,002
;     FILING DATE: 31-MAR-1994
;     APPLICATION NUMBER: US 08/307,619
;     FILING DATE: 16-SEP-1994
; ATTORNEY/AGENT INFORMATION:
;     NAME: Bartnicki, Audrey L.
;     REGISTRATION NUMBER: 40,499
;     REFERENCE/DOCKET NUMBER: 28111/32372A
; TELECOMMUNICATION INFORMATION:
;     TELEPHONE: 312-474-6300
; INFORMATION FOR SEQ ID NO: 342:
;     SEQUENCE CHARACTERISTICS:
;         LENGTH: 11 amino acids
;         TYPE: amino acid
;         STRANDEDNESS: single
;         TOPOLOGY: linear
;     SEQUENCE DESCRIPTION: SEQ ID NO: 342:
US-09-104-337A-342

```

```

Query Match          27.3%;  Score 3;  DB 4;  Length 11;
Best Local Similarity 100.0%;  Pred. No. 1.8e+03;
Matches      3;  Conservative    0;  Mismatches    0;  Indels      0;  Gaps      0;

```

Qy 4 SRD 6

Db

|||  
2 SRD 4

RESULT 58

US-09-104-337A-349

; Sequence 349, Application US/09104337A

; Patent No. 6492160

; GENERAL INFORMATION:

; APPLICANT: Winter, Gregory Paul

; Griffiths, Andrew David

; Williams, Samuel Cameron

; Waterhouse, Peter

; Nissim, Ahuva

; Johnson, Kevin Stuart

; Smith, Andrew John Hammond

; TITLE OF INVENTION: Methods for producing members of specific  
; binding pairs

; NUMBER OF SEQUENCES: 600

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Audrey L. Bartnicki

; STREET: Marshall, Gerstein & Borun

; 6300 Sears Tower, 233 South Wacker Drive

; CITY: Chicago

; STATE: Illinois

; COUNTRY: USA

; ZIP: 60606-6402

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/104,337A

; FILING DATE: 25-Jun-1998

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 08/350,260

; FILING DATE: 05-DEC-1994

; APPLICATION NUMBER: GB 9110549.4

; FILING DATE: 15-MAY-1991

; APPLICATION NUMBER: GB 9206318.9

; FILING DATE: 24-MAR-1992

; APPLICATION NUMBER: PCT/GB92/00883

; FILING DATE: 15-MAY-1992

; APPLICATION NUMBER: PCT/GB93/00605

; FILING DATE: 24-MAR-1993

; APPLICATION NUMBER: US 08/150,002

; FILING DATE: 31-MAR-1994

; APPLICATION NUMBER: US 08/307,619

; FILING DATE: 16-SEP-1994

; ATTORNEY/AGENT INFORMATION:

; NAME: Bartnicki, Audrey L.

; REGISTRATION NUMBER: 40,499

; REFERENCE/DOCKET NUMBER: 28111/32372A

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 312-474-6300

; INFORMATION FOR SEQ ID NO: 349:

; SEQUENCE CHARACTERISTICS:  
;  
; LENGTH: 11 amino acids  
;  
; TYPE: amino acid  
;  
; STRANDEDNESS: single  
;  
; TOPOLOGY: linear  
;  
; SEQUENCE DESCRIPTION: SEQ ID NO: 349:  
US-09-104-337A-349

Query Match 27.3%; Score 3; DB 4; Length 11;  
Best Local Similarity 100.0%; Pred. No. 1.8e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 SRD 6  
|||  
Db 2 SRD 4

RESULT 59

US-09-104-337A-375

; Sequence 375, Application US/09104337A  
; Patent No. 6492160  
; GENERAL INFORMATION:  
; APPLICANT: Winter, Gregory Paul  
; Griffiths, Andrew David  
; Williams, Samuel Cameron  
; Waterhouse, Peter  
; Nissim, Ahuva  
; Johnson, Kevin Stuart  
; Smith, Andrew John Hammond  
; TITLE OF INVENTION: Methods for producing members of specific  
; binding pairs  
; NUMBER OF SEQUENCES: 600  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Audrey L. Bartnicki  
; STREET: Marshall, Gerstein & Borun  
; 6300 Sears Tower, 233 South Wacker Drive  
; CITY: Chicago  
; STATE: Illinois  
; COUNTRY: USA  
; ZIP: 60606-6402  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/104,337A  
; FILING DATE: 25-Jun-1998  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/350,260  
; FILING DATE: 05-DEC-1994  
; APPLICATION NUMBER: GB 9110549.4  
; FILING DATE: 15-MAY-1991  
; APPLICATION NUMBER: GB 9206318.9  
; FILING DATE: 24-MAR-1992  
; APPLICATION NUMBER: PCT/GB92/00883  
; FILING DATE: 15-MAY-1992



; APPLICATION NUMBER: PCT/GB93/00605  
 ; FILING DATE: 24-MAR-1993  
 ; APPLICATION NUMBER: US 08/150,002  
 ; FILING DATE: 31-MAR-1994  
 ; APPLICATION NUMBER: US 08/307,619  
 ; FILING DATE: 16-SEP-1994  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: Bartnicki, Audrey L.  
 ; REGISTRATION NUMBER: 40,499  
 ; REFERENCE/DOCKET NUMBER: 28111/32372A  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: 312-474-6300  
 ; INFORMATION FOR SEQ ID NO: 375:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 11 amino acids  
 ; TYPE: amino acid  
 ; STRANDEDNESS: single  
 ; TOPOLOGY: linear  
 ; SEQUENCE DESCRIPTION: SEQ ID NO: 375:  
 US-09-104-337A-375

Query Match 27.3%; Score 3; DB 4; Length 11;  
 Best Local Similarity 100.0%; Pred. No. 1.8e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 SRD 6  
 |||  
 Db 2 SRD 4

# RESULT 60

US-09-104-337A-424

; Sequence 424, Application US/09104337A  
 ; Patent No. 6492160

## GENERAL INFORMATION:

; APPLICANT: Winter, Gregory Paul  
 ; Griffiths, Andrew David  
 ; Williams, Samuel Cameron  
 ; Waterhouse, Peter  
 ; Nissim, Ahuva  
 ; Johnson, Kevin Stuart  
 ; Smith, Andrew John Hammond

; TITLE OF INVENTION: Methods for producing members of specific  
 ; binding pairs

NUMBER OF SEQUENCES: 600

## CORRESPONDENCE ADDRESS:

; ADDRESSEE: Audrey L. Bartnicki  
 ; STREET: Marshall, Gerstein & Borun  
 ; 6300 Sears Tower, 233 South Wacker Drive  
 ; CITY: Chicago  
 ; STATE: Illinois  
 ; COUNTRY: USA  
 ; ZIP: 60606-6402

## COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS

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;      SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
;
;      CURRENT APPLICATION DATA:
;      APPLICATION NUMBER: US/09/104,337A
;      FILING DATE: 25-Jun-1998
;
;      PRIOR APPLICATION DATA:
;      APPLICATION NUMBER: US 08/350,260
;      FILING DATE: 05-DEC-1994
;      APPLICATION NUMBER: GB 9110549.4
;      FILING DATE: 15-MAY-1991
;      APPLICATION NUMBER: GB 9206318.9
;      FILING DATE: 24-MAR-1992
;      APPLICATION NUMBER: PCT/GB92/00883
;      FILING DATE: 15-MAY-1992
;      APPLICATION NUMBER: PCT/GB93/00605
;      FILING DATE: 24-MAR-1993
;      APPLICATION NUMBER: US 08/150,002
;      FILING DATE: 31-MAR-1994
;      APPLICATION NUMBER: US 08/307,619
;      FILING DATE: 16-SEP-1994
;
;      ATTORNEY/AGENT INFORMATION:
;      NAME: Bartnicki, Audrey L.
;      REGISTRATION NUMBER: 40,499
;      REFERENCE/DOCKET NUMBER: 28111/32372A
;
;      TELECOMMUNICATION INFORMATION:
;      TELEPHONE: 312-474-6300
;
;      INFORMATION FOR SEQ ID NO: 424:
;      SEQUENCE CHARACTERISTICS:
;      LENGTH: 11 amino acids
;      TYPE: amino acid
;      STRANDEDNESS: single
;      TOPOLOGY: linear
;
;      SEQUENCE DESCRIPTION: SEQ ID NO: 424:
US-09-104-337A-424

```

```

Query Match          27.3%; Score 3; DB 4; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches      3; Conservative      0; Mismatches      0; Indels      0; Gaps      0;

```

```

Qy      4 SRD 6
      |||
Db      2 SRD 4

```

```

RESULT 61
US-09-104-337A-427
; Sequence 427, Application US/09104337A
; Patent No. 6492160
; GENERAL INFORMATION:
; APPLICANT: Winter, Gregory Paul
; Griffiths, Andrew David
; Williams, Samuel Cameron
; Waterhouse, Peter
; Nissim, Ahuva
; Johnson, Kevin Stuart
; Smith, Andrew John Hammond
; TITLE OF INVENTION: Methods for producing members of specific
; binding pairs

```

```

; NUMBER OF SEQUENCES: 600
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Audrey L. Bartnicki
; STREET: Marshall, Gerstein & Borun
; 6300 Sears Tower, 233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606-6402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/104,337A
; FILING DATE: 25-Jun-1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/350,260
; FILING DATE: 05-DEC-1994
; APPLICATION NUMBER: GB 9110549.4
; FILING DATE: 15-MAY-1991
; APPLICATION NUMBER: GB 9206318.9
; FILING DATE: 24-MAR-1992
; APPLICATION NUMBER: PCT/GB92/00883
; FILING DATE: 15-MAY-1992
; APPLICATION NUMBER: PCT/GB93/00605
; FILING DATE: 24-MAR-1993
; APPLICATION NUMBER: US 08/150,002
; FILING DATE: 31-MAR-1994
; APPLICATION NUMBER: US 08/307,619
; FILING DATE: 16-SEP-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Bartnicki, Audrey L.
; REGISTRATION NUMBER: 40,499
; REFERENCE/DOCKET NUMBER: 28111/32372A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312-474-6300
; INFORMATION FOR SEQ ID NO: 427:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 427:
US-09-104-337A-427

```

```

Query Match          27.3%; Score 3; DB 4; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches      3; Conservative      0; Mismatches      0; Indels      0; Gaps      0;

```

```

QY      4 SRD 6
      |||
Db      2 SRD 4

```

RESULT 62

US-09-104-337A-430  
; Sequence 430, Application US/09104337A  
; Patent No. 6492160  
; GENERAL INFORMATION:  
; APPLICANT: Winter, Gregory Paul  
; Griffiths, Andrew David  
; Williams, Samuel Cameron  
; Waterhouse, Peter  
; Nissim, Ahuva  
; Johnson, Kevin Stuart  
; Smith, Andrew John Hammond  
; TITLE OF INVENTION: Methods for producing members of specific  
; binding pairs  
; NUMBER OF SEQUENCES: 600  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Audrey L. Bartnicki  
; STREET: Marshall, Gerstein & Borun  
; 6300 Sears Tower, 233 South Wacker Drive  
; CITY: Chicago  
; STATE: Illinois  
; COUNTRY: USA  
; ZIP: 60606-6402  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/104,337A  
; FILING DATE: 25-Jun-1998  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/350,260  
; FILING DATE: 05-DEC-1994  
; APPLICATION NUMBER: GB 9110549.4  
; FILING DATE: 15-MAY-1991  
; APPLICATION NUMBER: GB 9206318.9  
; FILING DATE: 24-MAR-1992  
; APPLICATION NUMBER: PCT/GB92/00883  
; FILING DATE: 15-MAY-1992  
; APPLICATION NUMBER: PCT/GB93/00605  
; FILING DATE: 24-MAR-1993  
; APPLICATION NUMBER: US 08/150,002  
; FILING DATE: 31-MAR-1994  
; APPLICATION NUMBER: US 08/307,619  
; FILING DATE: 16-SEP-1994  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Bartnicki, Audrey L.  
; REGISTRATION NUMBER: 40,499  
; REFERENCE/DOCKET NUMBER: 28111/32372A  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 312-474-6300  
; INFORMATION FOR SEQ ID NO: 430:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 11 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear

; SEQUENCE DESCRIPTION: SEQ ID NO: 430:  
US-09-104-337A-430

Query Match 27.3%; Score 3; DB 4; Length 11;  
Best Local Similarity 100.0%; Pred. No. 1.8e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 SRD 6  
|||  
Db 2 SRD 4

RESULT 63

US-09-104-337A-516

; Sequence 516, Application US/09104337A

; Patent No. 6492160

; GENERAL INFORMATION:

; APPLICANT: Winter, Gregory Paul  
; Griffiths, Andrew David  
; Williams, Samuel Cameron  
; Waterhouse, Peter  
; Nissim, Ahuva  
; Johnson, Kevin Stuart  
; Smith, Andrew John Hammond

; TITLE OF INVENTION: Methods for producing members of specific  
; binding pairs

; NUMBER OF SEQUENCES: 600

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Audrey L. Bartnicki  
; STREET: Marshall, Gerstein & Borun  
; 6300 Sears Tower, 233 South Wacker Drive  
; CITY: Chicago  
; STATE: Illinois  
; COUNTRY: USA  
; ZIP: 60606-6402

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/104,337A  
; FILING DATE: 25-Jun-1998

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 08/350,260  
; FILING DATE: 05-DEC-1994  
; APPLICATION NUMBER: GB 9110549.4  
; FILING DATE: 15-MAY-1991  
; APPLICATION NUMBER: GB 9206318.9  
; FILING DATE: 24-MAR-1992  
; APPLICATION NUMBER: PCT/GB92/00883  
; FILING DATE: 15-MAY-1992  
; APPLICATION NUMBER: PCT/GB93/00605  
; FILING DATE: 24-MAR-1993  
; APPLICATION NUMBER: US 08/150,002  
; FILING DATE: 31-MAR-1994  
; APPLICATION NUMBER: US 08/307,619

```

; FILING DATE: 16-SEP-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Bartnicki, Audrey L.
; REGISTRATION NUMBER: 40,499
; REFERENCE/DOCKET NUMBER: 28111/32372A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312-474-6300
; INFORMATION FOR SEQ ID NO: 516:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 516:
US-09-104-337A-516

```

```

Query Match          27.3%; Score 3; DB 4; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches      3; Conservative      0; Mismatches      0; Indels      0; Gaps      0;

```

```

Qy      4 SRD 6
        |||
Db      2 SRD 4

```

RESULT 64

US-09-104-337A-522

; Sequence 522, Application US/09104337A

; Patent No. 6492160

; GENERAL INFORMATION:

```

; APPLICANT: Winter, Gregory Paul
; Griffiths, Andrew David
; Williams, Samuel Cameron
; Waterhouse, Peter
; Nissim, Ahuva
; Johnson, Kevin Stuart
; Smith, Andrew John Hammond

```

; TITLE OF INVENTION: Methods for producing members of specific  
binding pairs

; NUMBER OF SEQUENCES: 600

; CORRESPONDENCE ADDRESS:

```

; ADDRESSEE: Audrey L. Bartnicki
; STREET: Marshall, Gerstein & Borun
;          6300 Sears Tower, 233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606-6402

```

; COMPUTER READABLE FORM:

```

; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)

```

; CURRENT APPLICATION DATA:

```

; APPLICATION NUMBER: US/09/104,337A
; FILING DATE: 25-Jun-1998

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; PRIOR APPLICATION DATA:

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; APPLICATION NUMBER: US 08/350,260
; FILING DATE: 05-DEC-1994
; APPLICATION NUMBER: GB 9110549.4
; FILING DATE: 15-MAY-1991
; APPLICATION NUMBER: GB 9206318.9
; FILING DATE: 24-MAR-1992
; APPLICATION NUMBER: PCT/GB92/00883
; FILING DATE: 15-MAY-1992
; APPLICATION NUMBER: PCT/GB93/00605
; FILING DATE: 24-MAR-1993
; APPLICATION NUMBER: US 08/150,002
; FILING DATE: 31-MAR-1994
; APPLICATION NUMBER: US 08/307,619
; FILING DATE: 16-SEP-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Bartnicki, Audrey L.
; REGISTRATION NUMBER: 40,499
; REFERENCE/DOCKET NUMBER: 28111/32372A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312-474-6300
; INFORMATION FOR SEQ ID NO: 522:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 522:
US-09-104-337A-522

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Query Match          27.3%; Score 3; DB 4; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches      3; Conservative      0; Mismatches      0; Indels      0; Gaps      0;

```

```

Qy      4 SRD 6
      |||
Db      2 SRD 4

```

```

RESULT 65
US-09-810-873-2
; Sequence 2, Application US/09810873
; Patent No. 6551599
; GENERAL INFORMATION:
; APPLICANT: Mandrell, David
; APPLICANT: Bates, Anna
; APPLICANT: Brandon, David
; TITLE OF INVENTION: Monoclonal Antibodies Against Campylobacter jejuni and
Campylobacter coli
; TITLE OF INVENTION: Outer Membrane Antigens
; FILE REFERENCE: Mandrell
; CURRENT APPLICATION NUMBER: US/09/810,873
; CURRENT FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 09/277,599
; PRIOR FILING DATE: 1999-03-26
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2

```

; LENGTH: 11  
; TYPE: PRT  
; ORGANISM: Campylobacter jejuni  
; FEATURE:  
; NAME/KEY: misc\_feature  
; LOCATION: ()..()  
; OTHER INFORMATION: The undetermined amino acid may or may not exist  
US-09-810-873-2

Query Match 27.3%; Score 3; DB 4; Length 11;  
Best Local Similarity 100.0%; Pred. No. 1.8e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 AIK 11  
|||  
Db 7 AIK 9

RESULT 66

US-08-488-446-550

; Sequence 550, Application US/08488446  
; Patent No. 6558898

; GENERAL INFORMATION:

; APPLICANT: JOHN N. SIMONS  
; APPLICANT: TAMI J. PILOT-MATIAS  
; APPLICANT: GEORGE J. DAWSON  
; APPLICANT: GEORGE G. SCHLAUDER  
; APPLICANT: SURESH M. DESAI  
; APPLICANT: THOMAS P. LEARY  
; APPLICANT: ANTHONY SCOTT MUEHROFF  
; APPLICANT: JAMES C. ERKER  
; APPLICANT: SHERI L. BUIJK  
; APPLICANT: ISA K. MUSHAWAR  
; TITLE OF INVENTION: NON-A, NON-B, NON-C, NON-D, NON-E HEPATITIS  
; TITLE OF INVENTION: REAGENTS AND METHODS FOR THEIR USE  
; NUMBER OF SEQUENCES: 716  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: ABBOTT LABORATORIES D377/AP6D  
; STREET: 100 ABBOTT PARK ROAD  
; CITY: ABBOTT PARK  
; STATE: IL  
; COUNTRY: USA  
; ZIP: 60064-3500

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/488,446  
; FILING DATE:  
; CLASSIFICATION:

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US/08/424,550  
; FILING DATE:

; ATTORNEY/AGENT INFORMATION:

; NAME: POREMBSKI, PRISCILLA E.



; REGISTRATION NUMBER: 33,207  
; REFERENCE/DOCKET NUMBER: 5527.PC.01  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 708-937-6365  
; TELEFAX: 708-938-2623  
; INFORMATION FOR SEQ ID NO: 550:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 11 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-08-488-446-550

Query Match 27.3%; Score 3; DB 4; Length 11;  
Best Local Similarity 100.0%; Pred. No. 1.8e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 AIK 11  
|||  
Db 2 AIK 4

RESULT 67

US-08-467-344A-550

; Sequence 550, Application US/08467344A  
; Patent No. 6586568

; GENERAL INFORMATION:

; APPLICANT: JOHN N. SIMONS  
; TAMI J. PILOT-MATIAS  
; GEORGE J. DAWSON  
; GEORGE G. SCHLAUDER  
; SURESH M. DESAI  
; THOMAS P. LEARY  
; ANTHONY SCOTT MUERHOFF  
; JAMES C. ERKER  
; SHERI L. BUIJK  
; ISA K. MUSHAHWAR

; TITLE OF INVENTION: NON-A, NON-B, NON-C, NON-D, NON-E HEPATITIS  
; REAGENTS AND METHODS FOR THEIR USE

; NUMBER OF SEQUENCES: 716

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: ABBOTT LABORATORIES D377/AP6D  
; STREET: 100 ABBOTT PARK ROAD  
; CITY: ABBOTT PARK  
; STATE: IL  
; COUNTRY: USA  
; ZIP: 60064-3500

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/467,344A  
; FILING DATE: 07-Jun-1995  
; CLASSIFICATION: <Unknown>

; PRIOR APPLICATION DATA:

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; APPLICATION NUMBER: 08/424,550
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: POREMBSKI, PRISCILLA E.
; REGISTRATION NUMBER: 33,207
; REFERENCE/DOCKET NUMBER: 5527.PC.01
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 708-937-6365
; TELEFAX: 708-938-2623
; INFORMATION FOR SEQ ID NO: 550:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 550:
US-08-467-344A-550

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Query Match          27.3%; Score 3; DB 4; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches      3; Conservative      0; Mismatches      0; Indels      0; Gaps      0;

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Qy      9 AIK 11
        |||
Db      2 AIK 4

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RESULT 68

US-09-079-030-55

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; Sequence 55, Application US/09079030
; Patent No. 6635623
; GENERAL INFORMATION:
; APPLICANT: Guevera, Jr., Juan G.
; APPLICANT: Hoogeveen, Ron C.
; APPLICANT: Moore, Paul J.
; TITLE OF INVENTION: LIPOPROTEINS AS NUCLEIC ACID DELIVERY
; TITLE OF INVENTION: VECTORS FOR TRANSFECTION OF EUKARYOTIC CELLS
; NUMBER OF SEQUENCES: 229
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold, White & Durkee
; STREET: P.O. Box 4433
; CITY: Houston
; STATE: Texas
; COUNTRY: USA
; ZIP: 77210
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/079,030
; FILING DATE: Concurrently Herewith
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: McMillian, Nabeela R.
; REGISTRATION NUMBER: P-43,363

```

; REFERENCE/DOCKET NUMBER: ARAG:003  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 512/418-3000  
; TELEFAX: 512/474-7577  
; INFORMATION FOR SEQ ID NO: 55:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 11 amino acids  
; TYPE: amino acid  
; STRANDEDNESS:  
; TOPOLOGY: linear  
US-09-079-030-55

Query Match 27.3%; Score 3; DB 4; Length 11;  
Best Local Similarity 100.0%; Pred. No. 1.8e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 AIK 11  
|||  
Db 4 AIK 6

RESULT 69

US-09-591-694-38

; Sequence 38, Application US/09591694  
; Patent No. 6638734  
; GENERAL INFORMATION:  
; APPLICANT: John C. Reed  
; APPLICANT: Shu-ichi Matsuzawa  
; TITLE OF INVENTION: Nucleic Acid Encoding Proteins Involved  
; TITLE OF INVENTION: in Protein Degradation, Products and Methods Related  
Thereto  
; FILE REFERENCE: P-LJ 4220  
; CURRENT APPLICATION NUMBER: US/09/591,694  
; CURRENT FILING DATE: 2000-06-09  
; EARLIER APPLICATION NUMBER: US 09/330,517  
; EARLIER FILING DATE: 1999-06-11  
; NUMBER OF SEQ ID NOS: 49  
; SOFTWARE: FastSEQ for Windows Version 4.0  
; SEQ ID NO 38  
; LENGTH: 11  
; TYPE: PRT  
; ORGANISM: Homo sapien  
US-09-591-694-38

Query Match 27.3%; Score 3; DB 4; Length 11;  
Best Local Similarity 100.0%; Pred. No. 1.8e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 AIK 11  
|||  
Db 2 AIK 4

RESULT 70

US-09-535-852-1119

; Sequence 1119, Application US/09535852  
; Patent No. 6638911

; GENERAL INFORMATION:  
; APPLICANT: Blachuk, Orest W.  
; APPLICANT: Symonds, James M.  
; APPLICANT: Gour, Barbara J.  
; TITLE OF INVENTION: COMPOUNDS AND EMTHODS FOR MODULATING  
; TITLE OF INVENTION: DESMOSOMAL CADHERIN-MEDIATED FUNCTIONS  
; FILE REFERENCE: 100086.407C6  
; CURRENT APPLICATION NUMBER: US/09/535,852  
; CURRENT FILING DATE: 2001-05-21  
; NUMBER OF SEQ ID NOS: 2009  
; SOFTWARE: FastSEQ for Windows Version 4.0  
; SEQ ID NO 1119  
; LENGTH: 11  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Cyclicized modulating agent comprising  
; OTHER INFORMATION: desmoglein-2 cell adhesion recognition sequence  
US-09-535-852-1119

Query Match 27.3%; Score 3; DB 4; Length 11;  
Best Local Similarity 100.0%; Pred. No. 1.8e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ARK 3  
|||  
Db 9 ARK 11

#### RESULT 71

US-09-535-852-1159  
; Sequence 1159, Application US/09535852  
; Patent No. 6638911  
; GENERAL INFORMATION:  
; APPLICANT: Blachuk, Orest W.  
; APPLICANT: Symonds, James M.  
; APPLICANT: Gour, Barbara J.  
; TITLE OF INVENTION: COMPOUNDS AND EMTHODS FOR MODULATING  
; TITLE OF INVENTION: DESMOSOMAL CADHERIN-MEDIATED FUNCTIONS  
; FILE REFERENCE: 100086.407C6  
; CURRENT APPLICATION NUMBER: US/09/535,852  
; CURRENT FILING DATE: 2001-05-21  
; NUMBER OF SEQ ID NOS: 2009  
; SOFTWARE: FastSEQ for Windows Version 4.0  
; SEQ ID NO 1159  
; LENGTH: 11  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Cyclicized modulating agent comprising  
; OTHER INFORMATION: desmoglein-2 cell adhesion recognition sequence  
US-09-535-852-1159

Query Match 27.3%; Score 3; DB 4; Length 11;  
Best Local Similarity 100.0%; Pred. No. 1.8e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ARK 3  
|||  
Db 9 ARK 11

RESULT 72

US-08-475-955-56

; Sequence 56, Application US/08475955

; Patent No. 6641813

; GENERAL INFORMATION:

; APPLICANT: Harley, John

; TITLE OF INVENTION: METHODS AND REAGENTS FOR DIAGNOSIS OF

; TITLE OF INVENTION: AUTOANTIBODIES

; NUMBER OF SEQUENCES: 218

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Patrea L. Pabst

; STREET: 2800 One Atlantic Center, 1250 West Peachtree Street

; CITY: Atlanta

; STATE: GA

; COUNTRY: USA

; ZIP: 30309-3450

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/475,955

; FILING DATE: June 7, 1995

; CLASSIFICATION: 424

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 07/867,819

; FILING DATE: April 13, 1992

; CLASSIFICATION: 424

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 07/648,205

; FILING DATE: January 31, 1991

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 07/472,947

; FILING DATE: January 31, 1990

; ATTORNEY/AGENT INFORMATION:

; NAME: Pabst, Patrea L.

; REGISTRATION NUMBER: 31,284

; REFERENCE/DOCKET NUMBER: OMRf114CIP(2)DIV

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (404)-873-8794

; TELEFAX: (404)-873-8795

; INFORMATION FOR SEQ ID NO: 56:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 11 amino acids

; TYPE: amino acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: peptide

; FEATURE:

; NAME/KEY: Binding-site

; LOCATION: 1..8

US-08-475-955-56

Query Match 27.3%; Score 3; DB 4; Length 11;  
Best Local Similarity 100.0%; Pred. No. 1.8e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 MTA 9  
|||  
Db 9 MTA 11

RESULT 73

US-09-775-052A-3

; Sequence 3, Application US/09775052A  
; Patent No. 6645501  
; GENERAL INFORMATION:  
; APPLICANT: Dowdy, Steven F.  
; TITLE OF INVENTION: ANTI-PATHOGEN SYSTEM AND METHODS OF USE THEREOF  
; FILE REFERENCE: 48881/1742  
; CURRENT APPLICATION NUMBER: US/09/775,052A  
; CURRENT FILING DATE: 2001-12-05  
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US/09/208,966  
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-12-10  
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/069,012  
; PRIOR FILING DATE: EARLIER FILING DATE: 1997-12-10  
; NUMBER OF SEQ ID NOS: 57  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 3  
; LENGTH: 11  
; TYPE: PRT  
; ORGANISM: human  
US-09-775-052A-3

Query Match 27.3%; Score 3; DB 4; Length 11;  
Best Local Similarity 100.0%; Pred. No. 1.8e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ARK 3  
|||  
Db 2 ARK 4

RESULT 74

US-09-576-824A-482

; Sequence 482, Application US/09576824A  
; Patent No. 6667387  
; GENERAL INFORMATION:  
; APPLICANT: De Leys, Robert  
; TITLE OF INVENTION: PROCESS FOR THE DETERMINATION OF PEPTIDES CORRESPONDING  
; TITLE OF INVENTION: TO IMMUNOLOGICALLY IMPORTANT EPITOPES AND THEIR USE IN  
; TITLE OF INVENTION: A PROCESS FOR DETERMINATION OF ANTIBODIES OF  
; TITLE OF INVENTION: BIOTINYLATED PEPTIDES CORRESPONDING TO IMMUNOLOGICALLY  
IMPORTANT  
; TITLE OF INVENTION: EPITOPES, A PROCESS FOR PREPARING THEM AND COMPOSITIONS  
; TITLE OF INVENTION: CONTAINING THEM  
; FILE REFERENCE: 2752-11  
; CURRENT APPLICATION NUMBER: US/09/576,824A

```

; CURRENT FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 08/723,425
; PRIOR FILING DATE: 1996-09-30
; PRIOR APPLICATION NUMBER: 09/146,028
; PRIOR FILING DATE: 1993-11-22
; PRIOR APPLICATION NUMBER: PCT/EP93/00517
; PRIOR FILING DATE: 1993-03-08
; PRIOR APPLICATION NUMBER: EP 92400598.6
; PRIOR FILING DATE: 1992-03-06
; NUMBER OF SEQ ID NOS: 600
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 482
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Hepatitis C virus
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: (1)
; OTHER INFORMATION: Xaa = modified site : when present, represents an
; OTHER INFORMATION: amino acid, amino group, or chemically modified
; OTHER INFORMATION: amino terminus
; NAME/KEY: VARIANT
; LOCATION: (11)
; OTHER INFORMATION: Xaa = modified site : when present, represents an
; OTHER INFORMATION: amino acid, OH-group, NH2-group, or a linkage
; OTHER INFORMATION: involv-ing these two groups
US-09-576-824A-482

```

```

Query Match          27.3%; Score 3; DB 4; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches      3; Conservative      0; Mismatches      0; Indels      0; Gaps      0;

```

```

Qy      1 ARK 3
      |||
Db      1 ARK 3

```

# RESULT 75

```

US-09-576-824A-546
; Sequence 546, Application US/09576824A
; Patent No. 6667387
; GENERAL INFORMATION:
; APPLICANT: De Leys, Robert
; TITLE OF INVENTION: PROCESS FOR THE DETERMINATION OF PEPTIDES CORRESPONDING
; TITLE OF INVENTION: TO IMMUNOLOGICALLY IMPORTANT EPITOPES AND THEIR USE IN
; TITLE OF INVENTION: A PROCESS FOR DETERMINATION OF ANTIBODIES OF
; TITLE OF INVENTION: BIOTINYLATED PEPTIDES CORRESPONDING TO IMMUNOLOGICALLY
IMPORTANT
; TITLE OF INVENTION: EPITOPES, A PROCESS FOR PREPARING THEM AND COMPOSITIONS
; TITLE OF INVENTION: CONTAINING THEM
; FILE REFERENCE: 2752-11
; CURRENT APPLICATION NUMBER: US/09/576,824A
; CURRENT FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 08/723,425
; PRIOR FILING DATE: 1996-09-30
; PRIOR APPLICATION NUMBER: 09/146,028
; PRIOR FILING DATE: 1993-11-22

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; PRIOR APPLICATION NUMBER: PCT/EP93/00517  
; PRIOR FILING DATE: 1993-03-08  
; PRIOR APPLICATION NUMBER: EP 92400598.6  
; PRIOR FILING DATE: 1992-03-06  
; NUMBER OF SEQ ID NOS: 600  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 546  
; LENGTH: 11  
; TYPE: PRT  
; ORGANISM: Hepatitis C virus  
; FEATURE:  
; NAME/KEY: VARIANT  
; LOCATION: (1)  
; OTHER INFORMATION: Xaa = modified site : when present, represents an  
; OTHER INFORMATION: amino acid, amino group, or chemically modified  
; OTHER INFORMATION: amino terminus  
; NAME/KEY: VARIANT  
; LOCATION: (11)  
; OTHER INFORMATION: Xaa = modified site : when present, represents an  
; OTHER INFORMATION: amino acid, OH-group, NH2-group, or a linkage  
; OTHER INFORMATION: involv-ing these two groups  
US-09-576-824A-546

Query Match 27.3%; Score 3; DB 4; Length 11;  
Best Local Similarity 100.0%; Pred. No. 1.8e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 RKS 4  
|||  
Db 8 RKS 10

Search completed: April 8, 2004, 15:52:17  
Job time : 12.3077 secs



OM protein - protein search, using sw model

Run on: April 8, 2004, 15:30:07 ; Search time 8.61538 Seconds  
 (without alignments)  
 122.816 Million cell updates/sec

Title: US-09-787-443A-22  
 Perfect score: 11  
 Sequence: 1 ARKSRDMTAAIK 11

Scoring table: OLIGO  
 Gapop 60.0 , Gapext 60.0

Searched: 283366 seqs, 96191526 residues

Word size : 0

Total number of hits satisfying chosen parameters: 226

Minimum DB seq length: 11  
 Maximum DB seq length: 11

Post-processing: Listing first 100 summaries

Database : PIR\_78:\*  
 1: pir1:\*  
 2: pir2:\*  
 3: pir3:\*  
 4: pir4:\*

Pred. No. is the number of results predicted by chance to have a  
 score greater than or equal to the score of the result being printed,  
 and is derived by analysis of the total score distribution.

# SUMMARIES

Result		%	Query				
No.	Score	Match	Length	DB	ID	Description	
1	3	27.3	11	2	PH0919	T-cell receptor be	
2	2	18.2	11	2	S32575	ribosomal protein	
3	2	18.2	11	2	A40693	transgelin - sheep	
4	2	18.2	11	2	A38841	rhodopsin homolog	
5	2	18.2	11	2	A26930	ermG leader peptid	
6	2	18.2	11	2	B26744	megascoliakinin -	
7	2	18.2	11	2	JQ0395	hypothetical prote	
8	2	18.2	11	2	S66606	quinoline 2-oxidor	
9	2	18.2	11	2	S58244	pyrroloquinoline q	
10	2	18.2	11	2	E60691	phycobilisome 8K 1	
11	2	18.2	11	2	PC2372	58K heat shock pro	
12	2	18.2	11	2	A44755	20alpha-hydroxyste	
13	2	18.2	11	2	S33519	probable secreted	

14	2	18.2	11	2	G61497	seed protein ws-23
15	2	18.2	11	2	PC4267	ribosomal protein
16	2	18.2	11	2	A38590	transforming prote
17	2	18.2	11	2	A34135	DNA-binding protei
18	2	18.2	11	2	A61512	variant surface gl
19	2	18.2	11	2	S05002	corazonin - Americ
20	2	18.2	11	2	S65395	chemical-sense-rel
21	2	18.2	11	2	E57789	gallbladder stone
22	2	18.2	11	2	S21727	gamma-interferon-i
23	2	18.2	11	2	PT0249	Ig heavy chain CRD
24	2	18.2	11	2	PT0273	Ig heavy chain CRD
25	2	18.2	11	2	S13279	Ile-Ser-bradykinin
26	2	18.2	11	2	S68637	acetylcholinestera
27	2	18.2	11	2	S54347	tubulin beta chain
28	2	18.2	11	2	PH1632	Ig H chain V-D-J r
29	2	18.2	11	2	PH1600	Ig H chain V-D-J r
30	2	18.2	11	2	PH1583	Ig H chain V-D-J r
31	2	18.2	11	2	PH1584	Ig H chain V-D-J r
32	2	18.2	11	2	PT0217	T-cell receptor be
33	2	18.2	11	2	PT0214	T-cell receptor be
34	2	18.2	11	2	C38887	T-cell receptor ga
35	2	18.2	11	2	PD0441	translation elonga
36	2	18.2	11	2	PH0929	T-cell receptor be
37	2	18.2	11	2	PH0947	T-cell receptor be
38	2	18.2	11	2	T12264	cytochrome-c oxida
39	2	18.2	11	2	T12253	cytochrome-c oxida
40	2	18.2	11	2	T12244	cytochrome-c oxida
41	2	18.2	11	2	T12248	cytochrome-c oxida
42	2	18.2	11	4	I52708	ELAV-like neuronal
43	2	18.2	11	4	S52252	hypothetical prote
44	1	9.1	11	1	XAVIBH	bradykinin-potenti
45	1	9.1	11	1	XASNBA	bradykinin-potenti
46	1	9.1	11	1	ECLQ2M	tachykinin II - mi
47	1	9.1	11	1	SPHO	substance P - hors
48	1	9.1	11	1	EOOCC	eledoisin - curled
49	1	9.1	11	1	A60654	substance P - guin
50	1	9.1	11	1	EOOC	eledoisin - musky
51	1	9.1	11	1	GMROL	leucosulfakinin -
52	1	9.1	11	1	LFTWWE	probable trpEG lea
53	1	9.1	11	2	S66196	alcohol dehydrogen
54	1	9.1	11	2	G42762	proteasome endopep
55	1	9.1	11	2	A33917	dihydroorotase (EC
56	1	9.1	11	2	B49164	chromogranin-B - r
57	1	9.1	11	2	JN0023	substance P - chic
58	1	9.1	11	2	PQ0682	photosystem I 17.5
59	1	9.1	11	2	S00616	parasporal crystal
60	1	9.1	11	2	C53652	rhlR protein - Pse
61	1	9.1	11	2	S09074	cytochrome P450-4b
62	1	9.1	11	2	A57458	gene Gax protein -
63	1	9.1	11	2	D60409	kassinin-like pept
64	1	9.1	11	2	F60409	substance P-like p
65	1	9.1	11	2	E60409	substance P-like p
66	1	9.1	11	2	YHRT	morphogenetic neur
67	1	9.1	11	2	YHHU	morphogenetic neur
68	1	9.1	11	2	YHBO	morphogenetic neur
69	1	9.1	11	2	YHXAE	morphogenetic neur
70	1	9.1	11	2	YHJFHY	morphogenetic neur

71	1	9.1	11	2	A61365	phyllokinin - Rohd
72	1	9.1	11	2	S23308	substance P - rain
73	1	9.1	11	2	S23306	substance P - Atla
74	1	9.1	11	2	B60409	kassinin-like pept
75	1	9.1	11	2	C60409	kassinin-like pept
76	1	9.1	11	2	S07203	uperolein - frog (
77	1	9.1	11	2	S07207	Crinia-angiotensin
78	1	9.1	11	2	S07201	physalaemin - frog
79	1	9.1	11	2	A61033	ranatachykinin A -
80	1	9.1	11	2	D61033	ranatachykinin D -
81	1	9.1	11	2	S42449	ant1 protein - pha
82	1	9.1	11	2	B58501	24K kidney and bla
83	1	9.1	11	2	D58502	27K bile and gallb
84	1	9.1	11	2	A58502	38K kidney stone p
85	1	9.1	11	2	C58501	42K bile stone pro
86	1	9.1	11	2	F58501	43.5K bile stone p
87	1	9.1	11	2	PQ0231	beta-glucosidase (
88	1	9.1	11	2	S04875	nifS protein - Bra
89	1	9.1	11	2	I41138	acetyl ornithine d
90	1	9.1	11	2	S42587	celF protein - Esc
91	1	9.1	11	2	S35490	type II site-speci
92	1	9.1	11	2	S21127	precorrin methyltr
93	1	9.1	11	2	S70720	trigger factor hom
94	1	9.1	11	2	S33782	acetolactate synth
95	1	9.1	11	2	B39853	LuxC protein - Pho
96	1	9.1	11	2	A58838	hemolysin - Porphy
97	1	9.1	11	2	B43669	hypothetical prote
98	1	9.1	11	2	D60691	phycobilisome 9K 1
99	1	9.1	11	2	PC2330	cycloinulooligosac
100	1	9.1	11	2	B41835	translation elonga

#### ALIGNMENTS

##### RESULT 1

PH0919

T-cell receptor beta chain V-D-J region (isolate 5) - rat (fragment)

C;Species: Rattus norvegicus (Norway rat)

C;Date: 09-Oct-1992 #sequence\_revision 09-Oct-1992 #text\_change 30-May-1997

C;Accession: PH0919

R;Gold, D.P.; Offner, H.; Sun, D.; Wiley, S.; Vandenbark, A.A.; Wilson, D.B.  
J. Exp. Med. 174, 1467-1476, 1991

A;Title: Analysis of T cell receptor beta chains in Lewis rats with experimental  
allergic encephalomyelitis: conserved complementarity determining region 3.

A;Reference number: PH0891; MUID:92078857; PMID:1836012

A;Accession: PH0919

A;Molecule type: mRNA

A;Residues: 1-11 <GOL>

A;Experimental source: concanavalin A-activated lymphoblast

A;Note: the authors translated the codon CAG for residue 11 as Glu

C;Keywords: T-cell receptor

Query Match 27.3%; Score 3; DB 2; Length 11;

Best Local Similarity 100.0%; Pred. No. 2.1e+03;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy            4 SRD 6  
              | | |  
Db            3 SRD 5

RESULT 2

S32575

ribosomal protein S2, plastid - squawroot plastid (fragment)

C;Species: plastid *Conopholis americana* (squawroot)

C;Date: 19-Mar-1997 #sequence\_revision 25-Apr-1997 #text\_change 13-Aug-1999

C;Accession: S32575

R;Taylor, G.W.; Wolfe, K.H.; Morden, C.W.; dePamphilis, C.W.; Palmer, J.D.

Curr. Genet. 20, 515-518, 1991

A;Title: Lack of a functional plastid tRNA(Cys) gene is associated with loss of photosynthesis in a lineage of parasitic plants.

A;Reference number: S32575; MUID:92145776; PMID:1723664

A;Accession: S32575

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-11 <TAY>

A;Cross-references: EMBL:X64567; NID:g11275; PIDN:CAA45868.1; PID:g11276

C;Genetics:

A;Gene: rps2

A;Genome: plastid

C;Superfamily: *Escherichia coli* ribosomal protein S2

C;Keywords: plastid; protein biosynthesis; ribosome

Query Match                    18.2%; Score 2; DB 2; Length 11;  
Best Local Similarity       100.0%; Pred. No. 2.6e+04;  
Matches       2; Conservative       0; Mismatches       0; Indels       0; Gaps       0;

Qy            7 MT 8  
              | |  
Db            1 MT 2

RESULT 3

A40693

transgelin - sheep (fragment)

C;Species: *Ovis orientalis aries*, *Ovis ammon aries* (domestic sheep)

C;Date: 03-May-1994 #sequence\_revision 03-May-1994 #text\_change 31-Oct-1997

C;Accession: A40693

R;Shapland, C.; Hsuan, J.J.; Totty, N.F.; Lawson, D.

J. Cell Biol. 121, 1065-1073, 1993

A;Title: Purification and properties of transgelin: a transformation and shape change sensitive actin-gelling protein.

A;Reference number: A40693; MUID:93273790; PMID:8501116

A;Accession: A40693

A;Molecule type: protein

A;Residues: 1-11 <SHA>

A;Experimental source: aorta

C;Comment: This protein gels actin and is down regulated by transformation or loss of cell adherence in culture.

C;Superfamily: smooth muscle protein SM22; calponin repeat homology; smooth muscle protein SM22 homology

C;Keywords: actin binding; cytoskeleton

Query Match 18.2%; Score 2; DB 2; Length 11;  
Best Local Similarity 100.0%; Pred. No. 2.6e+04;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 SR 5  
||  
Db 8 SR 9

RESULT 4

A38841

rhodopsin homolog - squid (*Watasenia scintillans*) (fragment)

N;Alternate names: visual pigment protein

C;Species: *Watasenia scintillans* (sparkling enope)

C;Date: 17-Jul-1992 #sequence\_revision 17-Jul-1992 #text\_change 31-Oct-1997

C;Accession: A38841

R;Seidou, M.; Kubota, I.; Hiraki, K.; Kito, Y.

Biochim. Biophys. Acta 957, 318-321, 1988

A;Title: Amino acid sequence of the retinal binding site of squid visual pigment.

A;Reference number: PT0063; MUID:89051045; PMID:3191148

A;Accession: A38841

A;Molecule type: protein

A;Residues: 1-11 <SEI>

C;Superfamily: vertebrate rhodopsin

C;Keywords: chromoprotein; retinal

F;3/Binding site: retinal (Lys) (covalent) #status experimental

Query Match 18.2%; Score 2; DB 2; Length 11;  
Best Local Similarity 100.0%; Pred. No. 2.6e+04;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 AI 10  
||  
Db 6 AI 7

RESULT 5

A26930

ermG leader peptide 1 - *Bacillus sphaericus*

C;Species: *Bacillus sphaericus*

C;Date: 08-Mar-1989 #sequence\_revision 08-Mar-1989 #text\_change 24-Sep-1999

C;Accession: A26930

R;Monod, M.; Mohan, S.; Dubnau, D.

J. Bacteriol. 169, 340-350, 1987

A;Title: Cloning and analysis of ermG, a new macrolide-lincosamide-streptogramin B resistance element from *Bacillus sphaericus*.

A;Reference number: A91840; MUID:87083389; PMID:3025178

A;Accession: A26930

A;Molecule type: DNA

A;Residues: 1-11 <MON>

A;Cross-references: GB:M15332; NID:g142881; PIDN:AAA22417.1; PID:g142882

C;Superfamily: unassigned leader peptides

Query Match 18.2%; Score 2; DB 2; Length 11;  
Best Local Similarity 100.0%; Pred. No. 2.6e+04;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 RD 6  
 ||  
Db 7 RD 8

RESULT 6

B26744

megascoliakinin - garden dagger wasp

N;Alternate names: 6-Thr-bradykinin-Lys-Ala

C;Species: Megascolia flavifrons (garden dagger wasp)

C;Date: 08-Mar-1989 #sequence\_revision 08-Mar-1989 #text\_change 18-Aug-2000

C;Accession: B26744; A28609

R;Yasuhara, T.; Mantel, P.; Nakajima, T.; Piek, T.

Toxicon 25, 527-535, 1987

A;Title: Two kinins isolated from an extract of the venom reservoirs of the solitary wasp Megascolia flavifrons.

A;Reference number: A94322; MUID:87293024; PMID:3617088

A;Accession: B26744

A;Molecule type: protein

A;Residues: 1-11 <YAS>

R;Nakajima, T.; Piek, T.; Yashuara, T.; Mantel, P.

Toxicon 26, 34, 1988

A;Title: Two kinins isolated from the venom of Megascolia flavifrons.

A;Reference number: A28609

A;Accession: A28609

A;Molecule type: protein

A;Residues: 1-11 <NAK>

C;Superfamily: unassigned animal peptides

C;Keywords: bradykinin; presynaptic neurotoxin; venom

Query Match 18.2%; Score 2; DB 2; Length 11;  
Best Local Similarity 100.0%; Pred. No. 2.6e+04;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 RK 3  
 ||  
Db 9 RK 10

RESULT 7

JQ0395

hypothetical protein (nodB 3' region) - Azorhizobium caulinodans

N;Alternate names: hypothetical 1.4K protein

C;Species: Azorhizobium caulinodans

A;Note: host Sesbania rostrata

C;Date: 07-Sep-1990 #sequence\_revision 07-Sep-1990 #text\_change 03-Feb-1994

C;Accession: JQ0395

R;Goethals, K.; Gao, M.; Tomekpe, K.; Van Montagu, M.; Holsters, M.

Mol. Gen. Genet. 219, 289-298, 1989

A;Title: Common nodABC genes in Nod locus 1 of Azorhizobium caulinodans: nucleotide sequence and plant-inducible expression.

A;Reference number: JQ0393; MUID:90136519; PMID:2615763

A;Accession: JQ0395

A;Molecule type: DNA

A;Residues: 1-11 <GOE>

A;Cross-references: GB:L18897

A;Experimental source: strain ORS571

Query Match 18.2%; Score 2; DB 2; Length 11;  
Best Local Similarity 100.0%; Pred. No. 2.6e+04;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AR 2  
||  
Db 10 AR 11

RESULT 8

S66606

quinoline 2-oxidoreductase alpha chain - Comamonas testosteroni (fragment)

C;Species: Comamonas testosteroni

C;Date: 15-Feb-1997 #sequence\_revision 13-Mar-1997 #text\_change 17-Mar-1999

C;Accession: S66606

R;Schach, S.; Tshisuaka, B.; Fetzner, S.; Lingens, F.

Eur. J. Biochem. 232, 536-544, 1995

A;Title: Quinoline 2-oxidoreductase and 2-oxo-1,2-dihydroquinoline 5,6-dioxygenase from Comamonas testosteroni 63. The first two enzymes in quinoline and 3-methylquinoline degradation.

A;Reference number: S66606; MUID:96035889; PMID:7556204

A;Accession: S66606

A;Molecule type: protein

A;Residues: 1-11 <SCH>

A;Experimental source: strain 63

Query Match 18.2%; Score 2; DB 2; Length 11;  
Best Local Similarity 100.0%; Pred. No. 2.6e+04;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 KS 4  
||  
Db 2 KS 3

RESULT 9

S58244

pyrroloquinoline quinone synthesis C - Pseudomonas fluorescens (fragment)

C;Species: Pseudomonas fluorescens

C;Date: 13-Jan-1996 #sequence\_revision 01-Mar-1996 #text\_change 08-Oct-1999

C;Accession: S58244

R;Schnider, U.; Keel, C.; Defago, G.; Haas, D.

submitted to the EMBL Data Library, May 1995

A;Description: Tn5-directed cloning of pqq genes from Pseudomonas fluorescens CHA0: their involvement in the production of the antibiotic pyoluteorin.

A;Reference number: S58239

A;Accession: S58244

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-11 <SCH>

A;Cross-references: EMBL:X87299; NID:g929799; PIDN:CAA60734.1; PID:g929806

Query Match 18.2%; Score 2; DB 2; Length 11;  
Best Local Similarity 100.0%; Pred. No. 2.6e+04;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 MT 8  
||  
Db 1 MT 2

RESULT 10

E60691

phycobilisome 8K linker protein - Synechococcus sp. (PCC 7002) (fragment)

C;Species: Synechococcus sp.

C;Date: 14-May-1993 #sequence\_revision 14-May-1993 #text\_change 07-May-1999

C;Accession: E60691

R;Bryant, D.A.; de Lorimier, R.; Guglielmi, G.; Stevens Jr., S.E.

Arch. Microbiol. 153, 550-560, 1990

A;Title: Structural and compositional analyses of the phycobilisomes of Synechococcus sp. PCC 7002. Analyses of the wild-type strain and a phycocyanin-less mutant constructed by interposon mutagenesis.

A;Reference number: A60691; MUID:90314662; PMID:2164365

A;Accession: E60691

A;Molecule type: protein

A;Residues: 1-11 <BRY>

C;Comment: This protein, one of the eleven components detected in this species of the phycobilisome that helps to trap light energy for photosystem II, does not carry a chromophore.

C;Keywords: photosystem II

Query Match 18.2%; Score 2; DB 2; Length 11;  
Best Local Similarity 100.0%; Pred. No. 2.6e+04;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 TA 9  
||  
Db 7 TA 8

RESULT 11

PC2372

58K heat shock protein groEL [similarity] - Bacillus cereus (strain ts-4) (fragment)

C;Species: Bacillus cereus

C;Date: 20-Apr-2000 #sequence\_revision 20-Apr-2000 #text\_change 20-Apr-2000

C;Accession: PC2372

R;Matsuno, K.; Miyamoto, T.; Yamaguchi, K.; Sayed, M.A.; Kajiwara, T.; Hatano, S.

Biosci. Biotechnol. Biochem. 59, 231-235, 1995

A;Title: Identification of DNA-binding proteins changed after induction of sporulation in Bacillus cereus.

A;Reference number: PC2369; MUID:95218265; PMID:7766022

A;Accession: PC2372

A;Status: preliminary

A;Molecule type: protein

A;Residues: 1-11 <MAS>

C;Keywords: heat shock; molecular chaperone; stress-induced protein

Query Match 18.2%; Score 2; DB 2; Length 11;  
Best Local Similarity 100.0%; Pred. No. 2.6e+04;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;



Qy 1 AR 2  
||  
Db 10 AR 11

RESULT 12

A44755

20alpha-hydroxysteroid dehydrogenase (EC 1.1.1.149) - Clostridium scindens (fragment)

C;Species: Clostridium scindens

C;Date: 12-Mar-1993 #sequence\_revision 12-Mar-1993 #text\_change 17-Mar-1999

C;Accession: A44755

R;Krafft, A.E.; Hylemon, P.B.

J. Bacteriol. 171, 2925-2932, 1989

A;Title: Purification and characterization of a novel form of 20alpha-hydroxysteroid dehydrogenase from Clostridium scindens.

A;Reference number: A44755; MUID:89255043; PMID:2722736

A;Accession: A44755

A;Molecule type: protein

A;Residues: 1-11 <KRA>

C;Comment: This enzyme was purified to homogeneity and shown to have 20alpha-hydroxysteroid dehydrogenase activity in the presence of NADH or NADPH. The enzyme as purified lacked glyceraldehyde-3-phosphate dehydrogenase (GAPDH) activity although the fragment shows near identify to known GAPDH sequences.

C;Keywords: homotetramer; NAD; NADP; oxidoreductase

Query Match 18.2%; Score 2; DB 2; Length 11;  
Best Local Similarity 100.0%; Pred. No. 2.6e+04;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 AI 10  
||  
Db 5 AI 6

RESULT 13

S33519

probable secreted protein - Acholeplasma laidlawii (fragment)

C;Species: Acholeplasma laidlawii

C;Date: 06-Jan-1995 #sequence\_revision 06-Jan-1995 #text\_change 22-Oct-1999

C;Accession: S33519

R;Boyer, M.J.; Jarhede, T.K.; Tegman, V.; Wieslander, A.

submitted to the EMBL Data Library, June 1993

A;Description: Sequence regions from Acholeplasma laidlawii which restore export of beta-lactamase in Escherichia coli.

A;Reference number: S33518

A;Accession: S33519

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-11 <BOY>

A;Cross-references: EMBL:Z22875; NID:g311706; PIDN:CAA80495.1; PID:g311708

Query Match 18.2%; Score 2; DB 2; Length 11;  
Best Local Similarity 100.0%; Pred. No. 2.6e+04;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 MT 8  
||  
Db 7 MT 8

RESULT 14

G61497

seed protein ws-23 - winged bean (fragment)

C;Species: Psophocarpus tetragonolobus (winged bean)

C;Date: 07-Oct-1994 #sequence\_revision 07-Oct-1994 #text\_change 07-Oct-1994

C;Accession: G61497

R;Hirano, H.

J. Protein Chem. 8, 115-130, 1989

A;Title: Microsequence analysis of winged bean seed proteins electroblotted from two-dimensional gel.

A;Reference number: A61491; MUID:89351606; PMID:2765119

A;Accession: G61497

A;Status: preliminary

A;Molecule type: protein

A;Residues: 1-11 <HIR>

C;Keywords: glycoprotein; seed

Query Match 18.2%; Score 2; DB 2; Length 11;  
Best Local Similarity 100.0%; Pred. No. 2.6e+04;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 KS 4  
||  
Db 2 KS 3

RESULT 15

PC4267

ribosomal protein L12.1 - rice (fragment)

C;Species: Oryza sativa (rice)

C;Date: 28-May-1997 #sequence\_revision 18-Jul-1997 #text\_change 18-Jul-1997

C;Accession: PC4267

R;Kawakami, T.; Kamo, M.; Chen, M.C.; Tsugita, A.

submitted to JIPID, April 1997

A;Reference number: PC4267

A;Accession: PC4267

A;Molecule type: protein

A;Residues: 1-11 <KAW>

A;Experimental source: strain Japonica Nihonbare

Query Match 18.2%; Score 2; DB 2; Length 11;  
Best Local Similarity 100.0%; Pred. No. 2.6e+04;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 TA 9  
||  
Db 2 TA 3

RESULT 16

A38590

transforming protein (Ddras) - slime mold (Dictyostelium discoideum) (fragment)

C;Species: Dictyostelium discoideum  
C;Date: 18-Oct-1991 #sequence\_revision 18-Oct-1991 #text\_change 30-Sep-1993  
C;Accession: A38590  
R;Esch, R.K.; Firtel, R.A.  
Genes Dev. 5, 9-21, 1991  
A;Title: cAMP and cell sorting control the spatial expression of a developmentally essential cell-type-specific ras gene in Dictyostelium.  
A;Reference number: A38590; MUID:91115102; PMID:1703508  
A;Accession: A38590  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-11 <ESC>  
A;Cross-references: GB:Z11804; GB:K02114; GB:X58190

Query Match 18.2%; Score 2; DB 2; Length 11;  
Best Local Similarity 100.0%; Pred. No. 2.6e+04;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 MT 8  
||  
Db 1 MT 2

RESULT 17

A34135

DNA-binding protein p - Crithidia fasciculata mitochondrion (fragment)

C;Species: mitochondrion Crithidia fasciculata

C;Date: 30-Sep-1991 #sequence\_revision 30-Sep-1991 #text\_change 07-Dec-1999

C;Accession: A34135

R;Tittawella, I.

FEBS Lett. 260, 57-61, 1990

A;Title: Kinetoplast DNA-aggregating proteins from the parasitic protozoan Crithidia fasciculata.

A;Reference number: A34135

A;Accession: A34135

A;Molecule type: protein

A;Residues: 1-11 <TIT>

C;Genetics:

A;Genome: mitochondrion

A;Genetic code: SGC6

C;Keywords: mitochondrion

Query Match 18.2%; Score 2; DB 2; Length 11;  
Best Local Similarity 100.0%; Pred. No. 2.6e+04;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 RK 3  
||  
Db 8 RK 9

RESULT 18

A61512

variant surface glycoprotein MITat 1.7 - Trypanosoma brucei (fragment)

C;Species: Trypanosoma brucei

C;Date: 28-Oct-1994 #sequence\_revision 28-Oct-1994 #text\_change 07-May-1999

C;Accession: A61512

R;Holder, A.A.; Cross, G.A.M.  
Mol. Biochem. Parasitol. 2, 135-150, 1981  
A;Title: Glycopeptides from variant surface glycoproteins of Trypanosoma brucei.  
C-terminal location of antigenically cross-reacting carbohydrate moieties.  
A;Reference number: A61512; MUID:81172836; PMID:6163983  
A;Accession: A61512  
A;Status: preliminary  
A;Molecule type: protein  
A;Residues: 1-11 <HOL>  
C;Keywords: glycoprotein

Query Match 18.2%; Score 2; DB 2; Length 11;  
Best Local Similarity 100.0%; Pred. No. 2.6e+04;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 TA 9  
||  
Db 2 TA 3

#### RESULT 19

S05002

corazonin - American cockroach

C;Species: Periplaneta americana (American cockroach)

C;Date: 07-Sep-1990 #sequence\_revision 09-Apr-1998 #text\_change 09-Apr-1998

C;Accession: S05002

R;Veenstra, J.A.

FEBS Lett. 250, 231-234, 1989

A;Title: Isolation and structure of corazonin, a cardioactive peptide from the american cockroach.

A;Reference number: S05002; MUID:89325572; PMID:2753132

A;Accession: S05002

A;Molecule type: protein

A;Residues: 1-11 <VEE>

C;Keywords: amidated carboxyl end; neuropeptide; pyroglutamic acid

F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental

F;11/Modified site: amidated carboxyl end (Asn) #status experimental

Query Match 18.2%; Score 2; DB 2; Length 11;  
Best Local Similarity 100.0%; Pred. No. 2.6e+04;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 SR 5  
||  
Db 6 SR 7

#### RESULT 20

S65395

chemical-sense-related lipophilic-ligand-binding protein - fruit fly (Drosophila melanogaster) (fragment)

C;Species: Drosophila melanogaster

C;Date: 28-Oct-1996 #sequence\_revision 13-Mar-1997 #text\_change 07-May-1999

C;Accession: S65395

R;Ozaki, M.; Morisaki, K.; Idei, W.; Ozaki, K.; Tokunaga, F.

Eur. J. Biochem. 230, 298-308, 1995

A;Title: A putative lipophilic stimulant carrier protein commonly found in the taste and olfactory systems. A unique member of the pheromone-binding protein superfamily.

A;Reference number: S65394; MUID:95324537; PMID:7601113

A;Accession: S65395

A;Status: preliminary

A;Molecule type: protein

A;Residues: 1-11 <OZA>

Query Match 18.2%; Score 2; DB 2; Length 11;  
Best Local Similarity 100.0%; Pred. No. 2.6e+04;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 RD 6

||

Db 6 RD 7

#### RESULT 21

E57789

gallbladder stone matrix protein, 25K - human (fragment)

C;Species: Homo sapiens (man)

C;Date: 23-Feb-1996 #sequence\_revision 23-Feb-1996 #text\_change 23-Feb-1996

C;Accession: E57789

R;Binette, J.P.; Binette, M.B.

submitted to the Protein Sequence Database, February 1996

A;Description: The proteins of gallbladder stones.

A;Reference number: A57789

A;Accession: E57789

A;Status: preliminary

A;Molecule type: protein

A;Residues: 1-11 <BIN>

Query Match 18.2%; Score 2; DB 2; Length 11;  
Best Local Similarity 100.0%; Pred. No. 2.6e+04;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 RK 3

||

Db 2 RK 3

#### RESULT 22

S21727

gamma-interferon-induced protein IP-30 precursor - human (fragment)

C;Species: Homo sapiens (man)

C;Date: 22-Nov-1993 #sequence\_revision 13-Mar-1997 #text\_change 13-Mar-1997

C;Accession: S21727

R;Wei, M.L.; Cresswell, P.

Nature 356, 443-446, 1992

A;Title: HLA-A2 molecules in an antigen-processing mutant cell contain signal sequence-derived peptides.

A;Reference number: S21727; MUID:92212461; PMID:1557127

A;Accession: S21727

A;Status: preliminary

A;Molecule type: protein

A;Residues: 1-11 <WEI>

Query Match 18.2%; Score 2; DB 2; Length 11;  
Best Local Similarity 100.0%; Pred. No. 2.6e+04;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 TA 9  
||  
Db 7 TA 8

RESULT 23

PT0249

Ig heavy chain CRD3 region (clone 2-109A) - human (fragment)

C;Species: Homo sapiens (man)

C;Date: 30-Sep-1993 #sequence\_revision 30-Sep-1993 #text\_change 16-Aug-1996

C;Accession: PT0249

R;Yamada, M.; Wasserman, R.; Reichard, B.A.; Shane, S.; Caton, A.J.; Rovera, G.  
J. Exp. Med. 173, 395-407, 1991

A;Title: Preferential utilization of specific immunoglobulin heavy chain  
diversity and joining segments in adult human peripheral blood B lymphocytes.

A;Reference number: PT0222; MUID:91108337; PMID:1899102

A;Accession: PT0249

A;Molecule type: DNA

A;Residues: 1-11 <YAM>

A;Experimental source: B lymphocyte

C;Keywords: heterotetramer; immunoglobulin

Query Match 18.2%; Score 2; DB 2; Length 11;  
Best Local Similarity 100.0%; Pred. No. 2.6e+04;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 RD 6  
||  
Db 7 RD 8

RESULT 24

PT0273

Ig heavy chain CRD3 region (clone 3-109A) - human (fragment)

C;Species: Homo sapiens (man)

C;Date: 30-Sep-1993 #sequence\_revision 30-Sep-1993 #text\_change 16-Aug-1996

C;Accession: PT0273

R;Yamada, M.; Wasserman, R.; Reichard, B.A.; Shane, S.; Caton, A.J.; Rovera, G.  
J. Exp. Med. 173, 395-407, 1991

A;Title: Preferential utilization of specific immunoglobulin heavy chain  
diversity and joining segments in adult human peripheral blood B lymphocytes.

A;Reference number: PT0222; MUID:91108337; PMID:1899102

A;Accession: PT0273

A;Molecule type: DNA

A;Residues: 1-11 <YAM>

A;Experimental source: B lymphocyte

C;Keywords: heterotetramer; immunoglobulin

Query Match 18.2%; Score 2; DB 2; Length 11;  
Best Local Similarity 100.0%; Pred. No. 2.6e+04;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 SR 5  
||  
Db 2 SR 3

RESULT 25

S13279

Ile-Ser-bradykinin - human (fragment)

N;Alternate names: T-kinin

C;Species: Homo sapiens (man)

C;Date: 02-Dec-1993 #sequence\_revision 13-Mar-1997 #text\_change 24-Jul-1998

C;Accession: S13279

R;Wunderer, G.; Walter, I.; Eschenbacher, B.; Lang, M.; Kellermann, J.;  
Kindermann, G.

Biol. Chem. Hoppe-Seyler 371, 977-981, 1990

A;Title: Ile-Ser-bradykinin is an aberrant permeability factor in various human  
malignant effusions.

A;Reference number: S13279; MUID:91166748; PMID:2076202

A;Accession: S13279

A;Molecule type: protein

A;Residues: 1-11 <WUN>

C;Keywords: bradykinin

Query Match 18.2%; Score 2; DB 2; Length 11;  
Best Local Similarity 100.0%; Pred. No. 2.6e+04;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 SR 5  
||  
Db 2 SR 3

RESULT 26

S68637

acetylcholinesterase (EC 3.1.1.7) P chain - bovine (fragment)

C;Species: Bos primigenius taurus (cattle)

C;Date: 04-Dec-1997 #sequence\_revision 04-Dec-1997 #text\_change 30-Jan-1998

C;Accession: S68637

R;Boschetti, N.; Brodbeck, U.

FEBS Lett. 380, 133-136, 1996

A;Title: The membrane anchor of mammalian brain acetylcholinesterase consists of  
a single glycosylated protein of 22 kDa.

A;Reference number: S68637; MUID:96181683; PMID:8603722

A;Accession: S68637

A;Molecule type: protein

A;Residues: 1-11 <BOS>

A;Experimental source: brain

C;Keywords: carboxylic ester hydrolase; glycoprotein; membrane protein

Query Match 18.2%; Score 2; DB 2; Length 11;  
Best Local Similarity 100.0%; Pred. No. 2.6e+04;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 KS 4  
||  
Db 4 KS 5

RESULT 27

S54347

tubulin beta chain - bovine (fragment)

C;Species: Bos primigenius taurus (cattle)

C;Date: 27-Oct-1995 #sequence\_revision 30-Jan-1998 #text\_change 07-May-1999

C;Accession: S54347

R;Okazaki, K.; Obata, N.H.; Inoue, S.; Hidaka, H.

Biochem. J. 306, 551-555, 1995

A;Title: S100-beta is a target protein of neurocalcin delta, an abundant isoform in glial cells.

A;Reference number: S54343; MUID:95194333; PMID:7887910

A;Accession: S54347

A;Molecule type: protein

A;Residues: 1-11 <OKA>

Query Match 18.2%; Score 2; DB 2; Length 11;  
Best Local Similarity 100.0%; Pred. No. 2.6e+04;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 AI 10

||

Db 6 AI 7

RESULT 28

PH1632

Ig H chain V-D-J region (clone B-less 209) - mouse (fragment)

C;Species: Mus musculus (house mouse)

C;Date: 02-Jun-1994 #sequence\_revision 02-Jun-1994 #text\_change 17-Mar-1999

C;Accession: PH1632

R;Levinson, D.A.; Campos-Torres, J.; Leder, P.

J. Exp. Med. 178, 317-329, 1993

A;Title: Molecular characterization of transgene-induced immunodeficiency in B-less mice using a novel quantitative limiting dilution polymerase chain reaction method.

A;Reference number: PH1580; MUID:93301609; PMID:8315387

A;Accession: PH1632

A;Molecule type: DNA

A;Residues: 1-11 <LEV>

A;Experimental source: bone marrow pre-B lymphocyte

C;Keywords: immunoglobulin

Query Match 18.2%; Score 2; DB 2; Length 11;  
Best Local Similarity 100.0%; Pred. No. 2.6e+04;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AR 2

||

Db 2 AR 3

RESULT 29

PH1600

Ig H chain V-D-J region (wild-type clone 310) - mouse (fragment)

C;Species: Mus musculus (house mouse)

C;Date: 02-Jun-1994 #sequence\_revision 02-Jun-1994 #text\_change 17-Mar-1999



C;Accession: PH1600  
R;Levinson, D.A.; Campos-Torres, J.; Leder, P.  
J. Exp. Med. 178, 317-329, 1993  
A;Title: Molecular characterization of transgene-induced immunodeficiency in B-less mice using a novel quantitative limiting dilution polymerase chain reaction method.  
A;Reference number: PH1580; MUID:93301609; PMID:8315387  
A;Accession: PH1600  
A;Molecule type: DNA  
A;Residues: 1-11 <LEV>  
A;Experimental source: bone marrow pre-B lymphocyte  
C;Keywords: immunoglobulin

Query Match 18.2%; Score 2; DB 2; Length 11;  
Best Local Similarity 100.0%; Pred. No. 2.6e+04;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AR 2  
||  
Db 2 AR 3

RESULT 30

PH1583

Ig H chain V-D-J region (wild-type clone 6) - mouse (fragment)

C;Species: Mus musculus (house mouse)

C;Date: 02-Jun-1994 #sequence\_revision 02-Jun-1994 #text\_change 17-Mar-1999

C;Accession: PH1583

R;Levinson, D.A.; Campos-Torres, J.; Leder, P.

J. Exp. Med. 178, 317-329, 1993

A;Title: Molecular characterization of transgene-induced immunodeficiency in B-less mice using a novel quantitative limiting dilution polymerase chain reaction method.

A;Reference number: PH1580; MUID:93301609; PMID:8315387

A;Accession: PH1583

A;Molecule type: DNA

A;Residues: 1-11 <LEV>

A;Experimental source: bone marrow pre-B lymphocyte

C;Keywords: immunoglobulin

Query Match 18.2%; Score 2; DB 2; Length 11;  
Best Local Similarity 100.0%; Pred. No. 2.6e+04;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AR 2  
||  
Db 2 AR 3

RESULT 31

PH1584

Ig H chain V-D-J region (wild-type clone 8) - mouse (fragment)

C;Species: Mus musculus (house mouse)

C;Date: 02-Jun-1994 #sequence\_revision 02-Jun-1994 #text\_change 17-Mar-1999

C;Accession: PH1584

R;Levinson, D.A.; Campos-Torres, J.; Leder, P.

J. Exp. Med. 178, 317-329, 1993

A;Title: Molecular characterization of transgene-induced immunodeficiency in B-less mice using a novel quantitative limiting dilution polymerase chain reaction method.

A;Reference number: PH1580; MUID:93301609; PMID:8315387

A;Accession: PH1584

A;Molecule type: DNA

A;Residues: 1-11 <LEV>

A;Experimental source: bone marrow pre-B lymphocyte

C;Keywords: immunoglobulin

Query Match 18.2%; Score 2; DB 2; Length 11;  
Best Local Similarity 100.0%; Pred. No. 2.6e+04;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AR 2  
||  
Db 2 AR 3

#### RESULT 32

PT0217

T-cell receptor beta chain V-J region (4-1-E.2) - mouse (fragment)

C;Species: Mus musculus (house mouse)

C;Date: 31-Dec-1991 #sequence\_revision 31-Dec-1991 #text\_change 30-May-1997

C;Accession: PT0217

R;Nakano, N.; Kikutani, H.; Nishimoto, H.; Kishimoto, T.

J. Exp. Med. 173, 1091-1097, 1991

A;Title: T cell receptor V gene usage of islet beta cell-reactive T cells is not restricted in non-obese diabetic mice.

A;Reference number: PT0209; MUID:91217621; PMID:1902501

A;Accession: PT0217

A;Molecule type: mRNA

A;Residues: 1-11 <NAK>

C;Keywords: T-cell receptor

Query Match 18.2%; Score 2; DB 2; Length 11;  
Best Local Similarity 100.0%; Pred. No. 2.6e+04;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 SR 5  
||  
Db 3 SR 4

#### RESULT 33

PT0214

T-cell receptor beta chain V-J region (4-1-L.6) - mouse (fragment)

C;Species: Mus musculus (house mouse)

C;Date: 31-Dec-1991 #sequence\_revision 31-Dec-1991 #text\_change 30-May-1997

C;Accession: PT0214

R;Nakano, N.; Kikutani, H.; Nishimoto, H.; Kishimoto, T.

J. Exp. Med. 173, 1091-1097, 1991

A;Title: T cell receptor V gene usage of islet beta cell-reactive T cells is not restricted in non-obese diabetic mice.

A;Reference number: PT0209; MUID:91217621; PMID:1902501

A;Accession: PT0214

A;Molecule type: mRNA

A;Residues: 1-11 <NAK>  
C;Keywords: T-cell receptor

Query Match 18.2%; Score 2; DB 2; Length 11;  
Best Local Similarity 100.0%; Pred. No. 2.6e+04;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AR 2  
||  
Db 3 AR 4

RESULT 34

C38887

T-cell receptor gamma chain (5a.3) - mouse (fragment)

C;Species: Mus musculus (house mouse)

C;Date: 03-Feb-1994 #sequence\_revision 03-Feb-1994 #text\_change 07-May-1999

C;Accession: C38887

R;Whetsell, M.; Mosley, R.L.; Whetsell, L.; Schaefer, F.V.; Miller, K.S.; Klein, J.R.

Mol. Cell. Biol. 11, 5902-5909, 1991

A;Title: Rearrangement and junctional-site sequence analyses of T-cell receptor gamma genes in intestinal intraepithelial lymphocytes from murine athymic chimeras.

A;Reference number: A41946; MUID:92049316; PMID:1658619

A;Accession: C38887

A;Status: preliminary; not compared with conceptual translation

A;Molecule type: DNA

A;Residues: 1-11 <WHE>

C;Keywords: T-cell receptor

Query Match 18.2%; Score 2; DB 2; Length 11;  
Best Local Similarity 100.0%; Pred. No. 2.6e+04;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 RD 6  
||  
Db 6 RD 7

RESULT 35

PD0441

translation elongation factor TU-like protein P43, mitochondrial - mouse (fragment)

C;Species: Mus musculus (house mouse)

C;Date: 21-Aug-1998 #sequence\_revision 21-Aug-1998 #text\_change 21-Aug-1998

C;Accession: PD0441

R;Kawakami, T.; Uchida, T.; Sakai, T.; Kamo, M.; Morimasa, T.; Tsugita, A. submitted to JIPID, August 1998

A;Description: Proteome analysis of mouse brain.

A;Reference number: PD0441

A;Accession: PD0441

A;Molecule type: protein

A;Residues: 1-11 <KAW>

A;Experimental source: striatum

C;Keywords: mitochondrion

Query Match 18.2%; Score 2; DB 2; Length 11;  
Best Local Similarity 100.0%; Pred. No. 2.6e+04;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 RD 6  
||  
Db 10 RD 11

RESULT 36

PH0929

T-cell receptor beta chain V-D-J region (clone 15) - rat (fragment)

C;Species: Rattus norvegicus (Norway rat)

C;Date: 09-Oct-1992 #sequence\_revision 09-Oct-1992 #text\_change 30-May-1997

C;Accession: PH0929

R;Gold, D.P.; Offner, H.; Sun, D.; Wiley, S.; Vandenbark, A.A.; Wilson, D.B.

J. Exp. Med. 174, 1467-1476, 1991

A;Title: Analysis of T cell receptor beta chains in Lewis rats with experimental allergic encephalomyelitis: conserved complementarity determining region 3.

A;Reference number: PH0891; MUID:92078857; PMID:1836012

A;Accession: PH0929

A;Molecule type: mRNA

A;Residues: 1-11 <GOL>

A;Experimental source: concanavalin A-activated lymphoblast

C;Keywords: T-cell receptor

Query Match 18.2%; Score 2; DB 2; Length 11;  
Best Local Similarity 100.0%; Pred. No. 2.6e+04;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 SR 5  
||  
Db 3 SR 4

RESULT 37

PH0947

T-cell receptor beta chain V-D-J region (clone A2) - rat (fragment)

C;Species: Rattus norvegicus (Norway rat)

C;Date: 09-Oct-1992 #sequence\_revision 09-Oct-1992 #text\_change 30-May-1997

C;Accession: PH0947

R;Gold, D.P.; Offner, H.; Sun, D.; Wiley, S.; Vandenbark, A.A.; Wilson, D.B.

J. Exp. Med. 174, 1467-1476, 1991

A;Title: Analysis of T cell receptor beta chains in Lewis rats with experimental allergic encephalomyelitis: conserved complementarity determining region 3.

A;Reference number: PH0891; MUID:92078857; PMID:1836012

A;Accession: PH0947

A;Molecule type: mRNA

A;Residues: 1-11 <GOL>

A;Experimental source: myelin basic protein fragment-reactive T-cell, recovered from experimentally induced allergic encephalomyelitis

C;Keywords: T-cell receptor

Query Match 18.2%; Score 2; DB 2; Length 11;  
Best Local Similarity 100.0%; Pred. No. 2.6e+04;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy            4 SR 5  
              ||  
Db            3 SR 4

RESULT 38

T12264

cytochrome-c oxidase (EC 1.9.3.1) chain I - *Laudakia caucasia* mitochondrion (fragment)

C;Species: mitochondrion *Laudakia caucasia*

C;Date: 23-Jul-1999 #sequence\_revision 23-Jul-1999 #text\_change 03-Aug-2001

C;Accession: T12264; T12267; T12270; T12273; T12276; T12279

R;Macey, J.R.; Schulte II, J.A.; Ananjeva, N.B.; Larson, A.; Rastegar-Pouyani, N.; Shammakov, S.M.; Papenfuss, T.J.

Mol. Phylogenet. Evol. 10, 118-131, 1998

A;Title: Phylogenetic relationships among agamid lizards of the *Laudakia caucasia* species group: Testing hypotheses of biogeographic fragmentation and an area cladogram for the Iranian Plateau.

A;Reference number: Z17470; MUID:98424476; PMID:9751922

A;Accession: T12264

A;Status: preliminary; translated from GB/EMBL/DDBJ

A;Molecule type: DNA

A;Residues: 1-11 <MAC1>

A;Cross-references: EMBL:AF028681; NID:g3641460; PIDN:AAC99596.1; PID:g3641463

A;Experimental source: specimen voucher CAS185010; California Academy of Sciences, San Francisco

A;Accession: T12267

A;Status: preliminary; translated from GB/EMBL/DDBJ

A;Molecule type: DNA

A;Residues: 1-11 <MAC2>

A;Cross-references: EMBL:AF028682; NID:g3641464; PIDN:AAC99599.1; PID:g3641467

A;Accession: T12270

A;Status: preliminary; translated from GB/EMBL/DDBJ

A;Molecule type: DNA

A;Residues: 1-11 <MAC3>

A;Cross-references: EMBL:AF028683; NID:g3641468; PIDN:AAC99602.1; PID:g3641471

A;Accession: T12273

A;Status: preliminary; translated from GB/EMBL/DDBJ

A;Molecule type: DNA

A;Residues: 1-11 <MAC4>

A;Cross-references: EMBL:AF028684; NID:g3641472; PIDN:AAC99605.1; PID:g3641475

A;Accession: T12276

A;Status: preliminary; translated from GB/EMBL/DDBJ

A;Molecule type: DNA

A;Residues: 1-11 <MAC5>

A;Cross-references: EMBL:AF028686; NID:g3641480; PIDN:AAC99611.1; PID:g3641483

A;Accession: T12279

A;Status: preliminary; translated from GB/EMBL/DDBJ

A;Molecule type: DNA

A;Residues: 1-11 <MAC6>

A;Cross-references: EMBL:AF028687; NID:g3641484; PIDN:AAC99614.1; PID:g3641487

C;Genetics:

A;Gene: COI

A;Genome: mitochondrion

C;Keywords: mitochondrion; oxidoreductase

Query Match

18.2%; Score 2; DB 2; Length 11;

Best Local Similarity 100.0%; Pred. No. 2.6e+04;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 MT 8  
||  
Db 4 MT 5

RESULT 39

T12253

cytochrome-c oxidase (EC 1.9.3.1) chain I - *Laudakia erythrogastra* mitochondrion (fragment)

C;Species: mitochondrion *Laudakia erythrogastra*

C;Date: 23-Jul-1999 #sequence\_revision 23-Jul-1999 #text\_change 03-Aug-2001

C;Accession: T12253; T12257

R;Macey, J.R.; Schulte II, J.A.; Ananjeva, N.B.; Larson, A.; Rastegar-Pouyani, N.; Shammakov, S.M.; Papenfuss, T.J.

Mol. Phylogenet. Evol. 10, 118-131, 1998

A;Title: Phylogenetic relationships among agamid lizards of the *Laudakia* caucasia species group: Testing hypotheses of biogeographic fragmentation and an area cladogram for the Iranian Plateau.

A;Reference number: Z17470; MUID:98424476; PMID:9751922

A;Accession: T12253

A;Status: preliminary; translated from GB/EMBL/DDBJ

A;Molecule type: DNA

A;Residues: 1-11 <MAC1>

A;Cross-references: EMBL:AF028679; NID:g3641452; PIDN:AAC99590.1; PID:g3641455

A;Experimental source: specimen voucher CAS182954; California Academy of Sciences, San Francisco

A;Accession: T12257

A;Status: preliminary; translated from GB/EMBL/DDBJ

A;Molecule type: DNA

A;Residues: 1-11 <MAC2>

A;Cross-references: EMBL:AF028680; NID:g3641456; PIDN:AAC99593.1; PID:g3641459

A;Experimental source: specimen voucher CAS184400; California Academy of Sciences, San Francisco

C;Genetics:

A;Gene: COI

A;Genome: mitochondrion

C;Keywords: mitochondrion; oxidoreductase

Query Match 18.2%; Score 2; DB 2; Length 11;  
Best Local Similarity 100.0%; Pred. No. 2.6e+04;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 MT 8  
||  
Db 4 MT 5

RESULT 40

T12244

cytochrome-c oxidase (EC 1.9.3.1) chain I - *Laudakia lehmanni* mitochondrion (fragment)

C;Species: mitochondrion *Laudakia lehmanni*

C;Date: 23-Jul-1999 #sequence\_revision 23-Jul-1999 #text\_change 03-Aug-2001

C;Accession: T12244

R;Macey, J.R.; Schulte II, J.A.; Ananjeva, N.B.; Larson, A.; Rastegar-Pouyani, N.; Shammakov, S.M.; Papenfuss, T.J.  
Mol. Phylogenet. Evol. 10, 118-131, 1998  
A;Title: Phylogenetic relationships among agamid lizards of the Laudakia caucasia species group: Testing hypotheses of biogeographic fragmentation and an area cladogram for the Iranian Plateau.  
A;Reference number: Z17470; MUID:98424476; PMID:9751922  
A;Accession: T12244  
A;Status: preliminary; translated from GB/EMBL/DDBJ  
A;Molecule type: DNA  
A;Residues: 1-11 <MAC>  
A;Cross-references: EMBL:AF028677; NID:g3641444; PID:g3641447; PIDN:AAC99584.1  
A;Experimental source: specimen voucher CAS183009; California Academy of Sciences, San Francisco  
C;Genetics:  
A;Gene: COI  
A;Genome: mitochondrion  
C;Keywords: mitochondrion; oxidoreductase

Query Match 18.2%; Score 2; DB 2; Length 11;  
Best Local Similarity 100.0%; Pred. No. 2.6e+04;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 MT 8  
||  
Db 4 MT 5

#### RESULT 41

T12248

cytochrome-c oxidase (EC 1.9.3.1) chain I - Laudakia microlepis mitochondrion (fragment)

C;Species: mitochondrion Laudakia microlepis

C;Date: 23-Jul-1999 #sequence\_revision 23-Jul-1999 #text\_change 03-Aug-2001

C;Accession: T12248

R;Macey, J.R.; Schulte II, J.A.; Ananjeva, N.B.; Larson, A.; Rastegar-Pouyani, N.; Shammakov, S.M.; Papenfuss, T.J.

Mol. Phylogenet. Evol. 10, 118-131, 1998

A;Title: Phylogenetic relationships among agamid lizards of the Laudakia caucasia species group: Testing hypotheses of biogeographic fragmentation and an area cladogram for the Iranian Plateau.

A;Reference number: Z17470; MUID:98424476; PMID:9751922

A;Accession: T12248

A;Status: preliminary; translated from GB/EMBL/DDBJ

A;Molecule type: DNA

A;Residues: 1-11 <MAC>

A;Cross-references: EMBL:AF028678; NID:g3641448; PID:g3641451; PIDN:AAC99587.1

A;Experimental source: specimen voucher GNM. RE. ex.-P120; Goteborg Natural History Museum Reptilia Exotica, Goteborg, Sweden

C;Genetics:

A;Gene: COI

A;Genome: mitochondrion

C;Keywords: mitochondrion; oxidoreductase

Query Match 18.2%; Score 2; DB 2; Length 11;  
Best Local Similarity 100.0%; Pred. No. 2.6e+04;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 MT 8  
||  
Db 4 MT 5

RESULT 42

I52708

ELAV-like neuronal protein 1, truncated splice form - human

N;Alternate names: Drosophila ELAV(embryonic lethal, abnormal vision)-like 4; Hu antigen D; paraneoplastic encephalomyelitis antigen

C;Species: Homo sapiens (man)

C;Date: 18-Aug-2000 #sequence\_revision 18-Aug-2000 #text\_change 18-Aug-2000

C;Accession: I52708

R;Sekido, Y.; Bader, S.A.; Carbone, D.P.; Johnson, B.E.; Minna, J.D.  
Cancer Res. 54, 4988-4992, 1994

A;Title: Molecular analysis of the HuD gene encoding a paraneoplastic encephalomyelitis antigen in human lung cancer cell lines.

A;Reference number: I52708; MUID:94349312; PMID:8069866

A;Accession: I52708

A;Status: translated from GB/EMBL/DDBJ

A;Molecule type: mRNA

A;Residues: 1-11 <SEK>

A;Cross-references: GB:S73887; NID:g688242; PIDN:AAD14142.1; PID:g4261842

C;Comment: This abnormal peptide is expressed. For the long splice form, see PIR:I38726.

C;Genetics:

A;Gene: GDB:ELAVL4; HUD; PNEM

A;Cross-references: GDB:141875; OMIM:168360

A;Map position: lp36-lp36

C;Keywords: alternative splicing

Query Match 18.2%; Score 2; DB 4; Length 11;  
Best Local Similarity 100.0%; Pred. No. 2.6e+04;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 SR 5  
||  
Db 5 SR 6

RESULT 43

S52252

hypothetical protein pco 5'-region - Escherichia coli plasmid pRJ1004 (fragment)

C;Species: Escherichia coli

C;Date: 22-Oct-1999 #sequence\_revision 22-Oct-1999 #text\_change 22-Oct-1999

C;Accession: S70166; S52252

R;Brown, N.L.; Barrett, S.R.; Camakaris, J.; Lee, B.T.O.; Rouch, D.A.  
Mol. Microbiol. 17, 1153-1166, 1995

A;Title: Molecular genetics and transport analysis of the copper-resistance determinant (pco) from Escherichia coli plasmid pRJ1004.

A;Reference number: S70159; MUID:96130847; PMID:8594334

A;Accession: S70166

A;Status: nucleic acid sequence not shown; translation not shown

A;Molecule type: DNA

A;Residues: 1-11 <BRO>

A;Cross-references: EMBL:X83541; NID:g619126; PIDN:CAA58524.1; PID:g619127



A;Note: the nucleotide sequence was submitted to the EMBL Data Library, January 1995

C;Comment: This is the hypothetical translation of a sequence that was not reported as a coding sequence in the complete genome.

C;Genetics:

A;Genome: plasmid pRJ1004

Query Match 18.2%; Score 2; DB 4; Length 11;  
Best Local Similarity 100.0%; Pred. No. 2.6e+04;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 TA 9  
||  
Db 6 TA 7

#### RESULT 44

XAVIBH

bradykinin-potentiating peptide - halys viper

N;Alternate names: BPP

C;Species: Agkistrodon halys (halys viper)

C;Date: 30-Sep-1988 #sequence\_revision 30-Sep-1988 #text\_change 05-Aug-1994

C;Accession: JC0002

R;Chi, C.W.; Wang, S.Z.; Xu, L.G.; Wang, M.Y.; Lo, S.S.; Huang, W.D.

Peptides 6, 339-342, 1985

A;Title: Structure-function studies on the bradykinin potentiating peptide from Chinese snake venom (Agkistrodon halys Pallas).

A;Reference number: JC0002; MUID:86177022; PMID:3008123

A;Accession: JC0002

A;Molecule type: protein

A;Residues: 1-11 <CHI>

C;Comment: Because this peptide both inhibits the activity of the angiotensin-converting enzyme and enhances the action of bradykinin, it is an antihypertensive agent.

C;Superfamily: bradykinin-potentiating peptide

C;Keywords: angiotensin-converting enzyme inhibitor; antihypertensive; bradykinin; pyroglutamic acid; venom

F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental

Query Match 9.1%; Score 1; DB 1; Length 11;  
Best Local Similarity 100.0%; Pred. No. 2e+05;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 R 2  
|  
Db 3 R 3

#### RESULT 45

XASNBA

bradykinin-potentiating peptide B - mamushi

C;Species: Agkistrodon blomhoffi (mamushi)

C;Date: 13-Jul-1981 #sequence\_revision 13-Jul-1981 #text\_change 08-Dec-1995

C;Accession: A01254

R;Kato, H.; Suzuki, T.

Proc. Jpn. Acad. 46, 176-181, 1970

A;Reference number: A01254

A;Accession: A01254  
A;Molecule type: protein  
A;Residues: 1-11 <KAT>  
A;Note: the sequence of the natural peptide was confirmed by the synthesis and analysis of a peptide having the identical structure and biological properties  
C;Superfamily: bradykinin-potentiating peptide  
C;Keywords: angiotensin-converting enzyme inhibitor; bradykinin; pyroglutamic acid; venom  
F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental

Query Match 9.1%; Score 1; DB 1; Length 11;  
Best Local Similarity 100.0%; Pred. No. 2e+05;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 R 2  
|  
Db 6 R 6

#### RESULT 46

ECLQ2M

tachykinin II - migratory locust

C;Species: Locusta migratoria (migratory locust)

C;Date: 31-Dec-1991 #sequence\_revision 31-Dec-1991 #text\_change 08-Dec-1995

C;Accession: S08266

R;Schoofs, L.; Holman, G.M.; Hayes, T.K.; Nachman, R.J.; de Loof, A.

FEBS Lett. 261, 397-401, 1990

A;Title: Locustatachykinin I and II, two novel insect neuropeptides with homology to peptides of the vertebrate tachykinin family.

A;Reference number: S08265; MUID:90184489; PMID:2311766

A;Accession: S08266

A;Molecule type: protein

A;Residues: 1-11 <SCH>

C;Superfamily: tachykinin

C;Keywords: amidated carboxyl end; neuropeptide; tachykinin

F;11/Modified site: amidated carboxyl end (Arg) #status experimental

Query Match 9.1%; Score 1; DB 1; Length 11;  
Best Local Similarity 100.0%; Pred. No. 2e+05;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 A 1  
|  
Db 1 A 1

#### RESULT 47

SPHO

substance P - horse

C;Species: Equus caballus (domestic horse)

C;Date: 23-Oct-1981 #sequence\_revision 23-Oct-1981 #text\_change 23-Aug-1996

C;Accession: A01558

R;Studer, R.O.; Trzeciak, A.; Lergier, W.

Helv. Chim. Acta 56, 860-866, 1973

A;Title: Isolierung und Aminosaeuresequenz von Substanz P aus Pferdedarm.

A;Reference number: A01558

A;Accession: A01558

A;Molecule type: protein  
A;Residues: 1-11 <STU>  
C;Superfamily: substance P precursor  
C;Keywords: amidated carboxyl end; hormone  
F;11/Modified site: amidated carboxyl end (Met) #status experimental

Query Match 9.1%; Score 1; DB 1; Length 11;  
Best Local Similarity 100.0%; Pred. No. 2e+05;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 R 2  
|  
Db 1 R 1

#### RESULT 48

EOOCC

eledoisin - curled octopus

C;Species: Eledone cirrosa, Ozaena cirrosa (curled octopus)

C;Date: 31-Dec-1991 #sequence\_revision 31-Dec-1991 #text\_change 20-Mar-1998

C;Accession: B01561; A01561

R;Anastasi, A.; Erspamer, V.

Arch. Biochem. Biophys. 101, 56-65, 1963

A;Title: The isolation and amino acid sequence of eledoisin, the active endecapeptide of the posterior salivary glands of Eledone.

A;Reference number: A01561

A;Accession: B01561

A;Molecule type: protein

A;Residues: 1-11 <ANA>

C;Superfamily: substance P precursor

C;Keywords: amidated carboxyl end; hormone; pyroglutamic acid; salivary gland; secretagogue; vasodilator; venom

F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental

F;11/Modified site: amidated carboxyl end (Met) #status experimental

Query Match 9.1%; Score 1; DB 1; Length 11;  
Best Local Similarity 100.0%; Pred. No. 2e+05;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 S 4  
|  
Db 3 S 3

#### RESULT 49

A60654

substance P - guinea pig

C;Species: Cavia porcellus (guinea pig)

C;Date: 14-May-1993 #sequence\_revision 27-Jun-1994 #text\_change 08-Dec-1995

C;Accession: A60654

R;Murphy, R.

Neuropeptides 14, 105-110, 1989

A;Title: Primary amino acid sequence of guinea-pig substance P.

A;Reference number: A60654; MUID:90044685; PMID:2478925

A;Accession: A60654

A;Molecule type: protein

A;Residues: 1-11 <MUR>

C;Superfamily: substance P precursor  
C;Keywords: amidated carboxyl end; neuropeptide; tachykinin  
F;11/Modified site: amidated carboxyl end (Met) #status experimental

Query Match 9.1%; Score 1; DB 1; Length 11;  
Best Local Similarity 100.0%; Pred. No. 2e+05;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 R 2  
|  
Db 1 R 1

#### RESULT 50

EOOC

eledoisin - musky octopus

C;Species: Eledone moschata, Ozaena moschata (musky octopus)

C;Date: 13-Jul-1981 #sequence\_revision 13-Jul-1981 #text\_change 20-Mar-1998

C;Accession: A01561

R;Anastasi, A.; Erspamer, V.

Arch. Biochem. Biophys. 101, 56-65, 1963

A;Title: The isolation and amino acid sequence of eledoisin, the active endecapeptide of the posterior salivary glands of Eledone.

A;Reference number: A01561

A;Accession: A01561

A;Molecule type: protein

A;Residues: 1-11 <ANA>

C;Superfamily: substance P precursor

C;Keywords: amidated carboxyl end; hormone; pyroglutamic acid; salivary gland; secretagogue; vasodilator; venom

F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental

F;11/Modified site: amidated carboxyl end (Met) #status experimental

Query Match 9.1%; Score 1; DB 1; Length 11;  
Best Local Similarity 100.0%; Pred. No. 2e+05;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 S 4  
|  
Db 3 S 3

#### RESULT 51

GMROL

leucosulfakinin - Madeira cockroach

N;Alternate names: LSK

C;Species: Leucophaea maderae (Madeira cockroach)

C;Date: 17-Mar-1987 #sequence\_revision 17-Mar-1987 #text\_change 13-Sep-1996

C;Accession: A01622

R;Nachman, R.J.; Holman, G.M.; Haddon, W.F.; Ling, N.

Science 234, 71-73, 1986

A;Title: Leucosulfakinin, a sulfated insect neuropeptide with homology to gastrin and cholecystokinin.

A;Reference number: A01622; MUID:86315858; PMID:3749893

A;Accession: A01622

A;Molecule type: protein

A;Residues: 1-11 <NAC>

C;Superfamily: gastrin  
C;Keywords: amidated carboxyl end; hormone; sulfoprotein  
F;6/Binding site: sulfate (Tyr) (covalent) #status experimental  
F;11/Modified site: amidated carboxyl end (Phe) #status experimental

Query Match 9.1%; Score 1; DB 1; Length 11;  
Best Local Similarity 100.0%; Pred. No. 2e+05;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 D 6  
|  
Db 5 D 5

#### RESULT 52

LFTWWE

probable trpEG leader peptide - *Thermus aquaticus*

C;Species: *Thermus aquaticus*

C;Date: 30-Jun-1991 #sequence\_revision 30-Jun-1991 #text\_change 16-Jul-1999

C;Accession: S03315

R;Sato, S.; Nakada, Y.; Kanaya, S.; Tanaka, T.

Biochim. Biophys. Acta 950, 303-312, 1988

A;Title: Molecular cloning and nucleotide sequence of *Thermus thermophilus* HB8 trpE and trpG.

A;Reference number: S03315; MUID:89000781; PMID:2844259

A;Accession: S03315

A;Molecule type: DNA

A;Residues: 1-11 <SAT>

A;Cross-references: EMBL:X07744; NID:g48261; PIDN:CAA30565.1; PID:g48262

A;Note: the source is designated as *Thermus thermophilus* HB8

C;Genetics:

A;Gene: trpL

C;Superfamily: probable trpEG leader peptide

Query Match 9.1%; Score 1; DB 1; Length 11;  
Best Local Similarity 100.0%; Pred. No. 2e+05;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 M 7  
|  
Db 1 M 1

#### RESULT 53

S66196

alcohol dehydrogenase (EC 1.1.1.1) class III high affinity form - cod (*Gadus* sp.) (fragment)

C;Species: *Gadus* sp. (cod)

C;Date: 14-Feb-1997 #sequence\_revision 13-Mar-1997 #text\_change 12-Jun-1998

C;Accession: S66196

R;Hjelmqvist, L.; Hackett, M.; Shafqat, J.; Danielsson, O.; Iida, J.; Hendrickson, R.C.; Michel, H.; Shabanowitz, J.; Hunt, D.F.; Joernvall, H. FEBS Lett. 367, 237-240, 1995

A;Title: Multiplicity of N-terminal structures of medium-chain alcohol dehydrogenases. Mass-spectrometric analysis of plant, lower vertebrate and higher vertebrate class I, II, and III forms of the enzyme.

A;Reference number: S66191; MUID:95331382; PMID:7607314

A;Accession: S66196  
A;Molecule type: protein  
A;Residues: 1-11 <HJE>  
C;Superfamily: alcohol dehydrogenase; long-chain alcohol dehydrogenase homology  
C;Keywords: alcohol metabolism; NAD; oxidoreductase

Query Match 9.1%; Score 1; DB 2; Length 11;  
Best Local Similarity 100.0%; Pred. No. 2e+05;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 T 8  
|  
Db 1 T 1

RESULT 54

G42762  
proteasome endopeptidase complex (EC 3.4.25.1) subunit 13 - bovine (fragment)  
C;Species: Bos primigenius taurus (cattle)  
C;Date: 04-Mar-1993 #sequence\_revision 18-Nov-1994 #text\_change 17-Feb-2003  
C;Accession: G42762  
R;Dick, L.R.; Moomaw, C.R.; Pramanik, B.C.; DeMartino, G.N.; Slaughter, C.A.  
Biochemistry 31, 7347-7355, 1992  
A;Title: Identification and localization of a cysteinyl residue critical for the  
trypsin-like catalytic activity of the proteasome.  
A;Reference number: A42762; MUID:92378961; PMID:1510924  
A;Accession: G42762  
A;Status: preliminary  
A;Molecule type: protein  
A;Residues: 1-11 <DIC>  
A;Note: sequence extracted from NCBI backbone (NCBIP:112176)  
C;Superfamily: multicatalytic endopeptidase complex chain C9  
C;Keywords: hydrolase

Query Match 9.1%; Score 1; DB 2; Length 11;  
Best Local Similarity 100.0%; Pred. No. 2e+05;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 M 7  
|  
Db 1 M 1

RESULT 55

A33917  
dihydroorotase (EC 3.5.2.3) - Chinese hamster (fragment)  
C;Species: Cricetulus griseus (Chinese hamster)  
C;Date: 09-Mar-1990 #sequence\_revision 09-Mar-1990 #text\_change 07-Nov-1997  
C;Accession: A33917  
R;Simmer, J.P.; Kelly, R.E.; Scully, J.L.; Grayson, D.R.; Rinker Jr., A.G.;  
Bergh, S.T.; Evans, D.R.  
Proc. Natl. Acad. Sci. U.S.A. 86, 4382-4386, 1989  
A;Title: Mammalian aspartate transcarbamylase (ATCase): sequence of the ATCase  
domain and interdomain linker in the CAD multifunctional polypeptide and  
properties of the isolated domain.  
A;Reference number: A33917; MUID:89282776; PMID:2543974  
A;Accession: A33917

A;Status: preliminary  
A;Molecule type: mRNA  
A;Residues: 1-11 <SIM>  
A;Cross-references: GB:M23652  
C;Superfamily: rudimentary enzyme; aspartate/ornithine carbamoyltransferase  
homology; Bacillus dihydroorotase homology; biotin carboxylase homology;  
carbamoyl-phosphate synthase (ammonia) homology; carbamoyl-phosphate synthase  
(glutamine-hydrolyzing) large chain homology; carbamoyl-phosphate synthase  
(glutamine-hydrolyzing) small chain homology; trpG homology  
C;Keywords: hydrolase

Query Match 9.1%; Score 1; DB 2; Length 11;  
Best Local Similarity 100.0%; Pred. No. 2e+05;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 R 2  
|  
Db 11 R 11

RESULT 56

B49164

chromogranin-B - rat (fragment)

C;Species: Rattus norvegicus (Norway rat)

C;Date: 19-Dec-1993 #sequence\_revision 18-Nov-1994 #text\_change 31-Oct-1997

C;Accession: B49164

R;Nielsen, E.; Welinder, B.S.; Madsen, O.D.

Endocrinology 129, 3147-3156, 1991

A;Title: Chromogranin-B, a putative precursor of eight novel rat glucagonoma  
peptides through processing at mono-, di-, or tribasic residues.

A;Reference number: A49164; MUID:92063871; PMID:1954895

A;Accession: B49164

A;Status: preliminary

A;Molecule type: protein

A;Residues: 1-11 <NIE>

A;Note: sequence extracted from NCBI backbone (NCBIP:66370)

C;Superfamily: chromogranin B precursor

Query Match 9.1%; Score 1; DB 2; Length 11;  
Best Local Similarity 100.0%; Pred. No. 2e+05;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 S 4  
|  
Db 3 S 3

RESULT 57

JN0023

substance P - chicken

C;Species: Gallus gallus (chicken)

C;Date: 07-Sep-1990 #sequence\_revision 07-Sep-1990 #text\_change 11-Jul-1997

C;Accession: JN0023

R;Conlon, J.M.; Katsoulis, S.; Schmidt, W.E.; Thim, L.

Regul. Pept. 20, 171-180, 1988

A;Title: [Arg3]substance P and neurokinin A from chicken small intestine.

A;Reference number: JN0023; MUID:88204263; PMID:2452461

A;Accession: JN0023  
A;Molecule type: protein  
A;Residues: 1-11 <CON>  
C;Superfamily: substance P precursor  
C;Keywords: amidated carboxyl end; tachykinin  
F;11/Modified site: amidated carboxyl end (Met) #status predicted

Query Match 9.1%; Score 1; DB 2; Length 11;  
Best Local Similarity 100.0%; Pred. No. 2e+05;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 R 2  
|  
Db 1 R 1

RESULT 58

PQ0682

photosystem I 17.5K D2 chain - common tobacco (fragment)

C;Species: Nicotiana tabacum (common tobacco)

C;Date: 19-May-1994 #sequence\_revision 19-May-1994 #text\_change 17-Mar-1999

C;Accession: PQ0682

R;Obokata, J.; Mikami, K.; Hayashida, N.; Nakamura, M.; Sugiura, M.

Plant Physiol. 102, 1259-1267, 1993

A;Title: Molecular heterogeneity of photosystem I. psaD, psaE, psaF, psaH and psaL are all present in isoforms in Nicotiana spp.

A;Reference number: PQ0667; MUID:94105345; PMID:8278548

A;Accession: PQ0682

A;Molecule type: protein

A;Residues: 1-11 <OBO>

C;Superfamily: photosystem I chain II

C;Keywords: chloroplast; photosynthesis; photosystem I; thylakoid

Query Match 9.1%; Score 1; DB 2; Length 11;  
Best Local Similarity 100.0%; Pred. No. 2e+05;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 A 1  
|  
Db 1 A 1

RESULT 59

S00616

parasporal crystal protein, wax moth-specific - Bacillus thuringiensis (strain galleriae 11-67) (fragment)

N;Alternate names: delta-endotoxin; parasporal crystal protein positive chain

C;Species: Bacillus thuringiensis

C;Date: 31-Dec-1988 #sequence\_revision 31-Dec-1988 #text\_change 13-Sep-1996

C;Accession: S00616

R;Chestukhina, G.G.; Kostina, L.I.; Zalunin, I.A.; Khodova, O.M.; Stepanov, V.M.

FEBS Lett. 232, 249-251, 1988

A;Title: Bacillus thuringiensis ssp. galleriae simultaneously produces two delta-endotoxins differing strongly in primary structure and entomocidal activity.

A;Reference number: S00615

A;Accession: S00616



A;Molecule type: protein  
A;Residues: 1-11 <CHE>  
C;Comment: This toxin is effective against the larvae of *Galleria melonella* (greater wax moth) but not those of *Lymantria dispar* (gypsy moth).  
C;Superfamily: parasporal crystal protein  
C;Keywords: delta-endotoxin

Query Match 9.1%; Score 1; DB 2; Length 11;  
Best Local Similarity 100.0%; Pred. No. 2e+05;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 A 1  
|  
Db 4 A 4

RESULT 60

C53652

rhlR protein - *Pseudomonas aeruginosa* (fragment)

C;Species: *Pseudomonas aeruginosa*

C;Date: 21-Jul-1995 #sequence\_revision 28-Jul-1995 #text\_change 21-Aug-1998

C;Accession: C53652

R;Ochsner, U.A.; Fiechter, A.; Reiser, J.

J. Biol. Chem. 269, 19787-19795, 1994

A;Title: Isolation, characterization, and expression in *Escherichia coli* of the *Pseudomonas aeruginosa* rhlAB genes encoding a rhamnosyltransferase involved in rhamnolipid biosurfactant synthesis.

A;Reference number: A53652; MUID:94327521; PMID:8051059

A;Accession: C53652

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-11 <OCH>

A;Cross-references: GB:L28170

C;Superfamily: sdiA regulatory protein

Query Match 9.1%; Score 1; DB 2; Length 11;  
Best Local Similarity 100.0%; Pred. No. 2e+05;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 M 7  
|  
Db 1 M 1

RESULT 61

S09074

cytochrome P450-4b - rat (fragment)

N;Alternate names: cytochrome P450K-5

N;Contains: oxidoreductase (EC 1.-.-.-)

C;Species: *Rattus norvegicus* (Norway rat)

C;Date: 23-Apr-1993 #sequence\_revision 23-Apr-1993 #text\_change 05-Mar-1999

C;Accession: S09074

R;Imaoka, S.; Terano, Y.; Funae, Y.

Arch. Biochem. Biophys. 278, 168-178, 1990

A;Title: Changes in the amount of cytochrome P450s in rat hepatic microsomes with starvation.

A;Reference number: S09072; MUID:90210577; PMID:2321956

A;Accession: S09074  
A;Molecule type: protein  
A;Residues: 1-11 <IMA>  
C;Superfamily: unassigned cytochrome P450; cytochrome P450 homology  
C;Keywords: heme; microsome; monooxygenase; oxidoreductase; transmembrane protein

Query Match 9.1%; Score 1; DB 2; Length 11;  
Best Local Similarity 100.0%; Pred. No. 2e+05;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 T 8  
|  
Db 5 T 5

RESULT 62

A57458

gene Gax protein - mouse (fragment)

C;Species: Mus sp. (mouse)

C;Date: 02-Jul-1996 #sequence\_revision 02-Jul-1996 #text\_change 15-Oct-1999

C;Accession: A57458

R;Andres, V.; Fisher, S.; Wearsch, P.; Walsh, K.

Mol. Cell. Biol. 15, 4272-4281, 1995

A;Title: Regulation of Gax homeobox gene transcription by a combination of positive factors including myocyte-specific enhancer factor 2.

A;Reference number: A57458; MUID:95349593; PMID:7623821

A;Accession: A57458

A;Status: preliminary; translated from GB/EMBL/DDBJ

A;Molecule type: DNA

A;Residues: 1-11 <RES>

A;Cross-references: GB:S79168; NID:g1050991

C;Genetics:

A;Gene: Gax

C;Superfamily: unassigned homeobox proteins; homeobox homology

C;Keywords: DNA binding; homeobox; nucleus; transcription regulation

Query Match 9.1%; Score 1; DB 2; Length 11;  
Best Local Similarity 100.0%; Pred. No. 2e+05;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 R 2  
|  
Db 10 R 10

RESULT 63

D60409

kassinin-like peptide K-III - frog (Pseudophryne guentheri)

C;Species: Pseudophryne guentheri

C;Date: 30-Jan-1993 #sequence\_revision 30-Jan-1993 #text\_change 02-Sep-2000

C;Accession: D60409

R;Simmaco, M.; Severini, C.; De Biase, D.; Barra, D.; Bossa, F.; Roberts, J.D.;

Melchiorri, P.; Erspamer, V.

Peptides 11, 299-304, 1990

A;Title: Six novel tachykinin- and bombesin-related peptides from the skin of the Australian frog Pseudophryne guentheri.

A;Reference number: A60409; MUID:90287814; PMID:2356157  
A;Accession: D60409  
A;Molecule type: protein  
A;Residues: 1-11 <SIM>  
C;Superfamily: unassigned animal peptides  
C;Keywords: amidated carboxyl end; pyroglutamic acid  
F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental  
F;11/Modified site: amidated carboxyl end (Met) #status experimental

Query Match 9.1%; Score 1; DB 2; Length 11;  
Best Local Similarity 100.0%; Pred. No. 2e+05;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 M 7  
|  
Db 11 M 11

RESULT 64

F60409

substance P-like peptide II - frog (*Pseudophryne guentheri*)

C;Species: *Pseudophryne guentheri*

C;Date: 30-Jan-1993 #sequence\_revision 30-Jan-1993 #text\_change 02-Sep-2000

C;Accession: F60409

R;Simmaco, M.; Severini, C.; De Biase, D.; Barra, D.; Bossa, F.; Roberts, J.D.;  
Melchiorri, P.; Erspamer, V.

Peptides 11, 299-304, 1990

A;Title: Six novel tachykinin- and bombesin-related peptides from the skin of  
the Australian frog *Pseudophryne guentheri*.

A;Reference number: A60409; MUID:90287814; PMID:2356157

A;Accession: F60409

A;Molecule type: protein

A;Residues: 1-11 <SIM>

C;Superfamily: unassigned animal peptides

C;Keywords: amidated carboxyl end; pyroglutamic acid

F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental

F;11/Modified site: amidated carboxyl end (Met) #status experimental

Query Match 9.1%; Score 1; DB 2; Length 11;  
Best Local Similarity 100.0%; Pred. No. 2e+05;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 M 7  
|  
Db 11 M 11

RESULT 65

E60409

substance P-like peptide I - frog (*Pseudophryne guentheri*)

C;Species: *Pseudophryne guentheri*

C;Date: 30-Jan-1993 #sequence\_revision 30-Jan-1993 #text\_change 02-Sep-2000

C;Accession: E60409

R;Simmaco, M.; Severini, C.; De Biase, D.; Barra, D.; Bossa, F.; Roberts, J.D.;  
Melchiorri, P.; Erspamer, V.

Peptides 11, 299-304, 1990

A;Title: Six novel tachykinin- and bombesin-related peptides from the skin of the Australian frog *Pseudophryne guentheri*.  
A;Reference number: A60409; MUID:90287814; PMID:2356157  
A;Accession: E60409  
A;Molecule type: protein  
A;Residues: 1-11 <SIM>  
C;Superfamily: unassigned animal peptides  
C;Keywords: amidated carboxyl end; pyroglutamic acid  
F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental  
F;11/Modified site: amidated carboxyl end (Met) #status experimental

Query Match 9.1%; Score 1; DB 2; Length 11;  
Best Local Similarity 100.0%; Pred. No. 2e+05;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 D 6  
|  
Db 5 D 5

#### RESULT 66

YHRT

morphogenetic neuropeptide - rat

C;Species: *Rattus norvegicus* (Norway rat)

C;Date: 20-Jun-2000 #sequence\_revision 20-Jun-2000 #text\_change 20-Jun-2000

C;Accession: A01427

R;Bodenmuller, H.; Schaller, H.C.

Nature 293, 579-580, 1981

A;Title: Conserved amino acid sequence of a neuropeptide, the head activator, from coelenterates to humans.

A;Reference number: A93266; MUID:82035850; PMID:7290191

A;Accession: A01427

A;Molecule type: protein

A;Residues: 1-11 <BOD>

R;Birrer, C.; Zachmann, B.; Bodenmuller, H.; Schaller, H.C.

FEBS Lett. 131, 317-321, 1981

A;Title: Synthesis of a new neuropeptide, the head activator from hydra.

A;Reference number: A91296; MUID:82050803; PMID:7297679

A;Contents: annotation; synthesis

A;Note: the synthetic peptide was identical with the natural peptide in chemical structure and biological activity

C;Comment: This peptide was first isolated from nerve cells of hydra and was called head activator by the authors, because it induced head-specific growth and differentiation in this animal. It has been found in mammalian intestine and hypothalamus.

C;Superfamily: unassigned animal peptides

C;Keywords: growth factor; hormone; hypothalamus; intestine; neuropeptide; pyroglutamic acid

F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental

Query Match 9.1%; Score 1; DB 2; Length 11;  
Best Local Similarity 100.0%; Pred. No. 2e+05;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 S 4  
|  
Db 6 S 6

# RESULT 67

YHHU

morphogenetic neuropeptide - human

C;Species: Homo sapiens (man)

C;Date: 20-Jun-2000 #sequence\_revision 20-Jun-2000 #text\_change 20-Jun-2000

C;Accession: B01427; A01427

R;Bodenmuller, H.; Schaller, H.C.

Nature 293, 579-580, 1981

A;Title: Conserved amino acid sequence of a neuropeptide, the head activator, from coelenterates to humans.

A;Reference number: A93266; MUID:82035850; PMID:7290191

A;Accession: B01427

A;Molecule type: protein

A;Residues: 1-11 <BOD>

R;Birrr, C.; Zachmann, B.; Bodenmuller, H.; Schaller, H.C.

FEBS Lett. 131, 317-321, 1981

A;Title: Synthesis of a new neuropeptide, the head activator from hydra.

A;Reference number: A91296; MUID:82050803; PMID:7297679

A;Contents: annotation; synthesis

A;Note: the synthetic peptide was identical with the natural peptide in chemical structure and biological activity

C;Comment: This peptide was first isolated from nerve cells of hydra and was called head activator because it induced head-specific growth and differentiation in this animal. It has been found in mammalian intestine and hypothalamus.

C;Superfamily: unassigned animal peptides

C;Keywords: blocked amino end; growth factor; hormone; hypothalamus; intestine; neuropeptide

F;1/Modified site: blocked amino end (Gln) (probably pyrrolidone carboxylic acid) #status experimental

Query Match 9.1%; Score 1; DB 2; Length 11;

Best Local Similarity 100.0%; Pred. No. 2e+05;

Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 S 4

|

Db 6 S 6

# RESULT 68

YHBO

morphogenetic neuropeptide - bovine

C;Species: Bos primigenius taurus (cattle)

C;Date: 20-Jun-2000 #sequence\_revision 20-Jun-2000 #text\_change 20-Jun-2000

C;Accession: C01427; A01427

R;Bodenmuller, H.; Schaller, H.C.

Nature 293, 579-580, 1981

A;Title: Conserved amino acid sequence of a neuropeptide, the head activator, from coelenterates to humans.

A;Reference number: A93266; MUID:82035850; PMID:7290191

A;Accession: C01427

A;Molecule type: protein

A;Residues: 1-11 <BOD>

R;Birrr, C.; Zachmann, B.; Bodenmuller, H.; Schaller, H.C.

FEBS Lett. 131, 317-321, 1981

A;Title: Synthesis of a new neuropeptide, the head activator from hydra.

A;Reference number: A91296; MUID:82050803; PMID:7297679

A;Contents: annotation; synthesis

A;Note: the synthetic peptide was identical with the natural peptide in chemical structure and biological activity

C;Comment: This peptide was first isolated from nerve cells of hydra and was called head activator because it induced head-specific growth and differentiation in this animal. It has been found in mammalian intestine and hypothalamus.

C;Superfamily: unassigned animal peptides

C;Keywords: blocked amino end; growth factor; hormone; hypothalamus; intestine; neuropeptide

F;1/Modified site: blocked amino end (Gln) (probably pyrrolidone carboxylic acid) #status experimental

Query Match 9.1%; Score 1; DB 2; Length 11;  
Best Local Similarity 100.0%; Pred. No. 2e+05;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 S 4

|

Db 6 S 6

#### RESULT 69

YHXAE

morphogenetic neuropeptide - sea anemone (*Anthopleura elegantissima*)

N;Alternate names: head activator

C;Species: *Anthopleura elegantissima*

C;Date: 20-Jun-2000 #sequence\_revision 20-Jun-2000 #text\_change 20-Jun-2000

C;Accession: A93900; A01427

R;Schaller, H.C.; Bodenmuller, H.

Proc. Natl. Acad. Sci. U.S.A. 78, 7000-7004, 1981

A;Title: Isolation and amino acid sequence of a morphogenetic peptide from hydra.

A;Reference number: A93900

A;Accession: A93900

A;Molecule type: protein

A;Residues: 1-11 <SCH>

R;Birrr, C.; Zachmann, B.; Bodenmuller, H.; Schaller, H.C.

FEBS Lett. 131, 317-321, 1981

A;Title: Synthesis of a new neuropeptide, the head activator from hydra.

A;Reference number: A91296; MUID:82050803; PMID:7297679

A;Contents: annotation; synthesis

A;Note: the synthetic peptide was identical with the natural peptide in chemical structure and biological activity

C;Comment: This peptide was first isolated from nerve cells of hydra and was called head activator because it induced head-specific growth and differentiation in this animal. It has also been found in mammalian intestine and hypothalamus.

C;Superfamily: unassigned animal peptides

C;Keywords: growth factor; hormone; neuropeptide; pyroglutamic acid

F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental

Query Match 9.1%; Score 1; DB 2; Length 11;  
Best Local Similarity 100.0%; Pred. No. 2e+05;

Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 S 4  
|  
Db 6 S 6

RESULT 70

YHJFHY

morphogenetic neuropeptide - Hydra attenuata

N;Alternate names: head activator

C;Species: Hydra attenuata

C;Date: 20-Jun-2000 #sequence\_revision 20-Jun-2000 #text\_change 20-Jun-2000

C;Accession: B93900; A01427

R;Schaller, H.C.; Bodenmuller, H.

Proc. Natl. Acad. Sci. U.S.A. 78, 7000-7004, 1981

A;Title: Isolation and amino acid sequence of a morphogenetic peptide from hydra.

A;Reference number: A93900

A;Accession: B93900

A;Molecule type: protein

A;Residues: 1-11 <SCH>

R;Birrr, C.; Zachmann, B.; Bodenmuller, H.; Schaller, H.C.

FEBS Lett. 131, 317-321, 1981

A;Title: Synthesis of a new neuropeptide, the head activator from hydra.

A;Reference number: A91296; MUID:82050803; PMID:7297679

A;Contents: annotation; synthesis

A;Note: the synthetic peptide was identical with the natural peptide in chemical structure and biological activity

C;Comment: This peptide was first isolated from nerve cells of hydra and was called head activator because it induced head-specific growth and differentiation in this animal. It has also been found in mammalian intestine and hypothalamus.

C;Superfamily: unassigned animal peptides

C;Keywords: growth factor; hormone; neuropeptide; pyroglutamic acid

F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental

Query Match 9.1%; Score 1; DB 2; Length 11;

Best Local Similarity 100.0%; Pred. No. 2e+05;

Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 S 4  
|  
Db 6 S 6

RESULT 71

A61365

phyllokinin - Rohde's leaf frog

N;Alternate names: bradykinyl-isoleucyl-tyrosine O-sulfate

C;Species: Phyllomedusa rohdei (Rohde's leaf frog)

C;Date: 09-Sep-1994 #sequence\_revision 09-Sep-1994 #text\_change 18-Aug-2000

C;Accession: A61365

R;Anastasi, A.; Bertaccini, G.; Erspamer, V.

Br. J. Pharmacol. 27, 479-485, 1966

A;Title: Pharmacological data on phyllokinin (bradykinyl-isoleucyl-tyrosine O-sulphate) and bradykinyl-isoleucyl-tyrosine.

A;Reference number: A61365; MUID:67179312; PMID:5970899  
A;Accession: A61365  
A;Status: preliminary  
A;Molecule type: protein  
A;Residues: 1-11 <ANA>  
C;Superfamily: unassigned animal peptides  
C;Keywords: sulfoprotein  
F;11/Binding site: sulfate (Tyr) (covalent) #status experimental

Query Match 9.1%; Score 1; DB 2; Length 11;  
Best Local Similarity 100.0%; Pred. No. 2e+05;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 R 2  
|  
Db 1 R 1

RESULT 72

S23308

substance P - rainbow trout

C;Species: Oncorhynchus mykiss (rainbow trout)

C;Date: 19-Mar-1997 #sequence\_revision 19-Mar-1997 #text\_change 18-Aug-2000

C;Accession: S23308

R;Jensen, J.; Conlon, J.M.

Eur. J. Biochem. 206, 659-664, 1992

A;Title: Substance-P-related and neurokinin-A-related peptides from the brain of the cod and trout.

A;Reference number: S23186; MUID:92298992; PMID:1376687

A;Accession: S23308

A;Molecule type: protein

A;Residues: 1-11 <JEN>

A;Experimental source: brain

C;Function:

A;Description: may play a physiological role in the regulation of cardiovascular and gastrointestinal functions

A;Note: substance P is derived by post-translational processing of preprotachykinin A

C;Superfamily: unassigned animal peptides

C;Keywords: neuropeptide; amidated carboxyl end; tachykinin

F;11/Modified site: amidated carboxyl end (Met) #status predicted

Query Match 9.1%; Score 1; DB 2; Length 11;  
Best Local Similarity 100.0%; Pred. No. 2e+05;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 K 3  
|  
Db 1 K 1

RESULT 73

S23306

substance P - Atlantic cod

C;Species: Gadus morhua (Atlantic cod)

C;Date: 19-Mar-1997 #sequence\_revision 19-Mar-1997 #text\_change 18-Aug-2000

C;Accession: S23306



R;Jensen, J.; Conlon, J.M.  
 Eur. J. Biochem. 206, 659-664, 1992  
 A;Title: Substance-P-related and neurokinin-A-related peptides from the brain of the cod and trout.  
 A;Reference number: S23186; MUJID:92298992; PMID:1376687  
 A;Accession: S23306  
 A;Molecule type: protein  
 A;Residues: 1-11 <JEN>  
 A;Experimental source: brain  
 C;Function:  
 A;Description: may play a physiological role in the regulation of cardiovascular and gastrointestinal functions  
 A;Note: substance P is derived by post-translational processing of preprotachykinin A  
 C;Superfamily: unassigned animal peptides  
 C;Keywords: neuropeptide; amidated carboxyl end; tachykinin  
 F;11/Modified site: amidated carboxyl end (Met) #status predicted

Query Match 9.1%; Score 1; DB 2; Length 11;  
 Best Local Similarity 100.0%; Pred. No. 2e+05;  
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 K 3  
 |  
 Db 1 K 1

#### RESULT 74

B60409  
 kassinin-like peptide K-I - frog (*Pseudophryne guentheri*)  
 C;Species: *Pseudophryne guentheri*  
 C;Date: 30-Jan-1993 #sequence\_revision 30-Jan-1993 #text\_change 18-Aug-2000  
 C;Accession: B60409  
 R;Simmaco, M.; Severini, C.; De Biase, D.; Barra, D.; Bossa, F.; Roberts, J.D.; Melchiorri, P.; Erspamer, V.  
 Peptides 11, 299-304, 1990  
 A;Title: Six novel tachykinin- and bombesin-related peptides from the skin of the Australian frog *Pseudophryne guentheri*.  
 A;Reference number: A60409; MUJID:90287814; PMID:2356157  
 A;Accession: B60409  
 A;Molecule type: protein  
 A;Residues: 1-11 <SIM>  
 A;Note: this peptide was also found in a deamidated form  
 C;Superfamily: unassigned animal peptides  
 C;Keywords: amidated carboxyl end; pyroglutamic acid  
 F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental  
 F;11/Modified site: amidated carboxyl end (Met) (partial) #status experimental

Query Match 9.1%; Score 1; DB 2; Length 11;  
 Best Local Similarity 100.0%; Pred. No. 2e+05;  
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 D 6  
 |  
 Db 5 D 5

RESULT 75

C60409

kassinin-like peptide K-II - frog (*Pseudophryne guentheri*)

C;Species: *Pseudophryne guentheri*

C;Date: 30-Jan-1993 #sequence\_revision 30-Jan-1993 #text\_change 18-Aug-2000

C;Accession: C60409

R;Simmaco, M.; Severini, C.; De Biase, D.; Barra, D.; Bossa, F.; Roberts, J.D.;  
Melchiorri, P.; Erspamer, V.

Peptides 11, 299-304, 1990

A;Title: Six novel tachykinin- and bombesin-related peptides from the skin of  
the Australian frog *Pseudophryne guentheri*.

A;Reference number: A60409; MUID:90287814; PMID:2356157

A;Accession: C60409

A;Molecule type: protein

A;Residues: 1-11 <SIM>

A;Note: this peptide was also found in a deamidated form

C;Superfamily: unassigned animal peptides

C;Keywords: amidated carboxyl end; pyroglutamic acid

F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental

F;11/Modified site: amidated carboxyl end (Met) (partial) #status experimental

Query Match 9.1%; Score 1; DB 2; Length 11;

Best Local Similarity 100.0%; Pred. No. 2e+05;

Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 D 6

|

Db 5 D 5

Search completed: April 8, 2004, 15:49:29

Job time : 9.61538 secs

OM protein - protein search, using sw model

Run on: April 8, 2004, 15:47:33 ; Search time 30.3077 Seconds  
(without alignments)  
95.432 Million cell updates/sec

Title: US-09-787-443A-22  
Perfect score: 11  
Sequence: 1 ARKSRDMTAIK 11

Scoring table: OLIGO  
Gapop 60.0 , Gapext 60.0

Searched: 1073127 seqs, 262937947 residues

Word size : 0

Total number of hits satisfying chosen parameters: 9223

Minimum DB seq length: 11

Maximum DB seq length: 11

Post-processing: Listing first 100 summaries

Database : Published\_Applications\_AA:\*

- 1: /cgn2\_6/ptodata/1/pubpaa/US07\_PUBCOMB.pep:\*
- 2: /cgn2\_6/ptodata/1/pubpaa/PCT\_NEW\_PUB.pep:\*
- 3: /cgn2\_6/ptodata/1/pubpaa/US06\_NEW\_PUB.pep:\*
- 4: /cgn2\_6/ptodata/1/pubpaa/US06\_PUBCOMB.pep:\*
- 5: /cgn2\_6/ptodata/1/pubpaa/US07\_NEW\_PUB.pep:\*
- 6: /cgn2\_6/ptodata/1/pubpaa/PCTUS\_PUBCOMB.pep:\*
- 7: /cgn2\_6/ptodata/1/pubpaa/US08\_NEW\_PUB.pep:\*
- 8: /cgn2\_6/ptodata/1/pubpaa/US08\_PUBCOMB.pep:\*
- 9: /cgn2\_6/ptodata/1/pubpaa/US09A\_PUBCOMB.pep:\*
- 10: /cgn2\_6/ptodata/1/pubpaa/US09B\_PUBCOMB.pep:\*
- 11: /cgn2\_6/ptodata/1/pubpaa/US09C\_PUBCOMB.pep:\*
- 12: /cgn2\_6/ptodata/1/pubpaa/US09\_NEW\_PUB.pep:\*
- 13: /cgn2\_6/ptodata/1/pubpaa/US10A\_PUBCOMB.pep:\*
- 14: /cgn2\_6/ptodata/1/pubpaa/US10B\_PUBCOMB.pep:\*
- 15: /cgn2\_6/ptodata/1/pubpaa/US10C\_PUBCOMB.pep:\*
- 16: /cgn2\_6/ptodata/1/pubpaa/US10\_NEW\_PUB.pep:\*
- 17: /cgn2\_6/ptodata/1/pubpaa/US60\_NEW\_PUB.pep:\*
- 18: /cgn2\_6/ptodata/1/pubpaa/US60\_PUBCOMB.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result	Query	
No.	Score Match Length DB ID	Description

1	4	36.4	11	12	US-10-344-878-5	Sequence 5, Appli
2	4	36.4	11	12	US-10-344-878-6	Sequence 6, Appli
3	3	27.3	11	8	US-08-424-550B-550	Sequence 550, App
4	3	27.3	11	9	US-09-935-682-19	Sequence 19, Appl
5	3	27.3	11	9	US-09-935-682-56	Sequence 56, Appl
6	3	27.3	11	9	US-09-813-653-22	Sequence 22, Appl
7	3	27.3	11	9	US-09-817-661-19	Sequence 19, Appl
8	3	27.3	11	9	US-09-873-676-4	Sequence 4, Appli
9	3	27.3	11	9	US-09-810-873-2	Sequence 2, Appli
10	3	27.3	11	9	US-09-758-128-25	Sequence 25, Appl
11	3	27.3	11	9	US-09-758-128-28	Sequence 28, Appl
12	3	27.3	11	9	US-09-949-196-16	Sequence 16, Appl
13	3	27.3	11	9	US-09-071-838-212	Sequence 212, App
14	3	27.3	11	9	US-09-758-426-25	Sequence 25, Appl
15	3	27.3	11	9	US-09-758-426-28	Sequence 28, Appl
16	3	27.3	11	9	US-09-758-198-25	Sequence 25, Appl
17	3	27.3	11	9	US-09-758-198-28	Sequence 28, Appl
18	3	27.3	11	10	US-09-983-802-567	Sequence 567, App
19	3	27.3	11	10	US-09-882-291-44	Sequence 44, Appl
20	3	27.3	11	10	US-09-861-661-25	Sequence 25, Appl
21	3	27.3	11	10	US-09-861-661-28	Sequence 28, Appl
22	3	27.3	11	10	US-09-809-391-698	Sequence 698, App
23	3	27.3	11	10	US-09-775-052-3	Sequence 3, Appli
24	3	27.3	11	10	US-09-847-946A-126	Sequence 126, App
25	3	27.3	11	10	US-09-847-946A-127	Sequence 127, App
26	3	27.3	11	10	US-09-880-748-3177	Sequence 3177, Ap
27	3	27.3	11	10	US-09-876-904A-33	Sequence 33, Appl
28	3	27.3	11	10	US-09-876-904A-236	Sequence 236, App
29	3	27.3	11	10	US-09-876-904A-509	Sequence 509, App
30	3	27.3	11	10	US-09-972-656-6	Sequence 6, Appli
31	3	27.3	11	10	US-09-802-083-10	Sequence 10, Appl
32	3	27.3	11	10	US-09-882-171-698	Sequence 698, App
33	3	27.3	11	12	US-09-973-278-398	Sequence 398, App
34	3	27.3	11	12	US-10-362-527-63	Sequence 63, Appl
35	3	27.3	11	12	US-10-430-685-39	Sequence 39, Appl
36	3	27.3	11	12	US-10-398-616-4	Sequence 4, Appli
37	3	27.3	11	12	US-10-398-616-10	Sequence 10, Appl
38	3	27.3	11	12	US-09-912-609-27	Sequence 27, Appl
39	3	27.3	11	14	US-10-060-019-1	Sequence 1, Appli
40	3	27.3	11	14	US-10-211-069-56	Sequence 56, Appl
41	3	27.3	11	14	US-10-062-710-168	Sequence 168, App
42	3	27.3	11	14	US-10-229-915-21	Sequence 21, Appl
43	3	27.3	11	14	US-10-227-616-68	Sequence 68, Appl
44	3	27.3	11	14	US-10-211-088-202	Sequence 202, App
45	3	27.3	11	14	US-10-136-738-2	Sequence 2, Appli
46	3	27.3	11	14	US-10-213-512-212	Sequence 212, App
47	3	27.3	11	14	US-10-165-732A-10	Sequence 10, Appl
48	3	27.3	11	14	US-10-172-785-10	Sequence 10, Appl
49	3	27.3	11	14	US-10-322-210-4	Sequence 4, Appli
50	3	27.3	11	14	US-10-077-065-2	Sequence 2, Appli
51	3	27.3	11	14	US-10-304-443-4	Sequence 4, Appli
52	3	27.3	11	14	US-10-008-524A-171	Sequence 171, App
53	3	27.3	11	14	US-10-168-445-83	Sequence 83, Appl
54	3	27.3	11	14	US-10-405-339-13	Sequence 13, Appl
55	3	27.3	11	15	US-10-376-121A-56	Sequence 56, Appl
56	3	27.3	11	15	US-10-350-719-171	Sequence 171, App

57	3	27.3	11	15	US-10-378-173-136	Sequence 136, App
58	3	27.3	11	15	US-10-032-037B-5	Sequence 5, Appli
59	3	27.3	11	15	US-10-032-037B-118	Sequence 118, App
60	3	27.3	11	15	US-10-032-037B-131	Sequence 131, App
61	3	27.3	11	15	US-10-032-037B-133	Sequence 133, App
62	3	27.3	11	15	US-10-032-037B-139	Sequence 139, App
63	3	27.3	11	15	US-10-032-037B-161	Sequence 161, App
64	3	27.3	11	15	US-10-032-037B-202	Sequence 202, App
65	3	27.3	11	15	US-10-029-988B-5	Sequence 5, Appli
66	3	27.3	11	15	US-10-029-988B-118	Sequence 118, App
67	3	27.3	11	15	US-10-029-988B-131	Sequence 131, App
68	3	27.3	11	15	US-10-029-988B-133	Sequence 133, App
69	3	27.3	11	15	US-10-029-988B-139	Sequence 139, App
70	3	27.3	11	15	US-10-029-988B-161	Sequence 161, App
71	3	27.3	11	15	US-10-029-988B-202	Sequence 202, App
72	3	27.3	11	15	US-10-032-423A-5	Sequence 5, Appli
73	3	27.3	11	15	US-10-032-423A-118	Sequence 118, App
74	3	27.3	11	15	US-10-032-423A-131	Sequence 131, App
75	3	27.3	11	15	US-10-032-423A-133	Sequence 133, App
76	3	27.3	11	15	US-10-032-423A-139	Sequence 139, App
77	3	27.3	11	15	US-10-032-423A-161	Sequence 161, App
78	3	27.3	11	15	US-10-032-423A-202	Sequence 202, App
79	3	27.3	11	15	US-10-014-099F-30	Sequence 30, Appl
80	3	27.3	11	15	US-10-149-138-552	Sequence 552, App
81	3	27.3	11	15	US-10-149-138-620	Sequence 620, App
82	3	27.3	11	15	US-10-149-138-1270	Sequence 1270, Ap
83	3	27.3	11	15	US-10-350-367-36	Sequence 36, Appl
84	2	18.2	11	8	US-08-450-842-46	Sequence 46, Appl
85	2	18.2	11	8	US-08-996-470-2	Sequence 2, Appli
86	2	18.2	11	8	US-08-424-550B-192	Sequence 192, App
87	2	18.2	11	8	US-08-424-550B-523	Sequence 523, App
88	2	18.2	11	8	US-08-841-636A-28	Sequence 28, Appl
89	2	18.2	11	8	US-08-817-832B-10	Sequence 10, Appl
90	2	18.2	11	8	US-08-765-837-15	Sequence 15, Appl
91	2	18.2	11	8	US-08-344-824-24	Sequence 24, Appl
92	2	18.2	11	9	US-09-222-179-1	Sequence 1, Appli
93	2	18.2	11	9	US-09-045-620-1	Sequence 1, Appli
94	2	18.2	11	9	US-09-113-924-18	Sequence 18, Appl
95	2	18.2	11	9	US-09-113-924-22	Sequence 22, Appl
96	2	18.2	11	9	US-09-739-907-108	Sequence 108, App
97	2	18.2	11	9	US-09-826-210-4	Sequence 4, Appli
98	2	18.2	11	9	US-09-770-621-37	Sequence 37, Appl
99	2	18.2	11	9	US-09-802-077-14	Sequence 14, Appl
100	2	18.2	11	9	US-09-802-077-33	Sequence 33, Appl

#### ALIGNMENTS

##### RESULT 1

US-10-344-878-5

; Sequence 5, Application US/10344878

; Publication No. US20040053848A1

; GENERAL INFORMATION:

; APPLICANT: The University of Virginia Patent Foundation

; APPLICANT: Allis, C. David

; APPLICANT: Strahl, Brian D

```
; TITLE OF INVENTION: Antibodies Specific for Methylated Lysines in Histones
; FILE REFERENCE: 00601-02
; CURRENT APPLICATION NUMBER: US/10/344,878
; CURRENT FILING DATE: 2003-08-14
; PRIOR APPLICATION NUMBER: US 60/227,767
; PRIOR FILING DATE: 2000-08-25
; PRIOR APPLICATION NUMBER: US 60/302,747
; PRIOR FILING DATE: 2001-07-03
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 5
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: synthetic peptide used to raise antibodies against the H3
amino t
; OTHER INFORMATION: erminus having MeLys at the fifth amino acid position.
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (5)..(5)
; OTHER INFORMATION: METHYLATION
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: (10)..(11)
; OTHER INFORMATION: artificial amino acids added to the natural histone
sequence to a
; OTHER INFORMATION: id in the production of the antibody
US-10-344-878-5
```

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Query Match          36.4%; Score 4; DB 12; Length 11;
Best Local Similarity 100.0%; Pred. No. 5e+02;
Matches      4; Conservative      0; Mismatches      0; Indels      0; Gaps      0;
```

```
Qy      1 ARKS 4
        ||||
Db      3 ARKS 6
```

## RESULT 2

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US-10-344-878-6
; Sequence 6, Application US/10344878
; Publication No. US20040053848A1
; GENERAL INFORMATION:
; APPLICANT: The University of Virginia Patent Foundation
; APPLICANT: Allis, C. David
; APPLICANT: Strahl, Brian D
; TITLE OF INVENTION: Antibodies Specific for Methylated Lysines in Histones
; FILE REFERENCE: 00601-02
; CURRENT APPLICATION NUMBER: US/10/344,878
; CURRENT FILING DATE: 2003-08-14
; PRIOR APPLICATION NUMBER: US 60/227,767
; PRIOR FILING DATE: 2000-08-25
; PRIOR APPLICATION NUMBER: US 60/302,747
; PRIOR FILING DATE: 2001-07-03
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: PatentIn version 3.1
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; SEQ ID NO 6
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: synthetic peptide used to raise antibodies against the H3
amino t
; OTHER INFORMATION: erminus having MeLys at the fifth amino acid position.
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (5)..(5)
; OTHER INFORMATION: METHYLATION
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: (10)..(11)
; OTHER INFORMATION: artificial amino acids added to the natural histone
sequence to a
; OTHER INFORMATION: id in the production of the antibody
US-10-344-878-6
```

```
Query Match          36.4%; Score 4; DB 12; Length 11;
Best Local Similarity 100.0%; Pred. No. 5e+02;
Matches      4; Conservative      0; Mismatches      0; Indels      0; Gaps      0;
```

```
Qy          1 ARKS 4
            ||||
Db          3 ARKS 6
```

# RESULT 3

US-08-424-550B-550

```
; Sequence 550, Application US/08424550B
; Publication No. US20020119447A1
; GENERAL INFORMATION:
; APPLICANT: JOHN N. SIMONS
; APPLICANT: TAMI J. PILOT-MATIAS
; APPLICANT: GEORGE J. DAWSON
; APPLICANT: GEORGE G. SCHLAUDER
; APPLICANT: SURESH M. DESAI
; APPLICANT: THOMAS P. LEARY
; APPLICANT: ANTHONY SCOTT MUEERHOFF
; APPLICANT: JAMES C. ERKER
; APPLICANT: SHERI L. BUIJK
; APPLICANT: ISA K. MUSHAHWAR
; TITLE OF INVENTION: NON-A, NON-B. NON-C, NON-D, NON-E HEPATITIS
; TITLE OF INVENTION: REAGENTS AND METHODS FOR THEIR USE
; NUMBER OF SEQUENCES: 716
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: ABBOTT LABORATORIES D377/AP6D
; STREET: 100 ABBOTT PARK ROAD
; CITY: ABBOTT PARK
; STATE: IL
; COUNTRY: USA
; ZIP: 60064-3500
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
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```

;   OPERATING SYSTEM:  PC-DOS/MS-DOS
;   SOFTWARE:  PatentIn Release #1.0, Version #1.25
;   CURRENT APPLICATION DATA:
;   APPLICATION NUMBER:  US/08/424,550B
;   FILING DATE:
;   CLASSIFICATION:  435435
;   ATTORNEY/AGENT INFORMATION:
;   NAME:  POREMBSKI, PRISCILLA E.
;   REGISTRATION NUMBER:  33,207
;   REFERENCE/DOCKET NUMBER:  5527.PC.01
;   TELECOMMUNICATION INFORMATION:
;   TELEPHONE:  708-937-6365
;   TELEFAX:  708-938-2623
;   INFORMATION FOR SEQ ID NO:  550:
;   SEQUENCE CHARACTERISTICS:
;   LENGTH:  11 amino acids
;   TYPE:  amino acid
;   TOPOLOGY:  linear
;   MOLECULE TYPE:  protein
US-08-424-550B-550

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```

Query Match          27.3%;  Score 3;  DB 8;  Length 11;
Best Local Similarity 100.0%;  Pred. No. 6.4e+03;
Matches      3;  Conservative    0;  Mismatches    0;  Indels      0;  Gaps      0;

```

```

Qy          9 AIK 11
            |||
Db          2 AIK 4

```

#### RESULT 4

```

US-09-935-682-19
; Sequence 19, Application US/09935682
; Patent No. US20020059032A1
; GENERAL INFORMATION:
; APPLICANT: Societe de Conseils de Recherches et D'Applications Scientifiques
; APPLICANT: Ferrer, Camara Y.
; TITLE OF INVENTION: Rational Selection of Putative Peptides from Identified
Nucleotide or
; TITLE OF INVENTION:  Peptide Sequences
; FILE REFERENCE: 58767.000005
; CURRENT APPLICATION NUMBER: US/09/935,682
; CURRENT FILING DATE: 2001-08-24
; PRIOR APPLICATION NUMBER: 09/257,525
; PRIOR FILING DATE: 1999-02-25
; PRIOR APPLICATION NUMBER: PCT/FR00/00460
; PRIOR FILING DATE: 2000-02-24
; NUMBER OF SEQ ID NOS: 73
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 19
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-935-682-19

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```

Query Match          27.3%;  Score 3;  DB 9;  Length 11;
Best Local Similarity 100.0%;  Pred. No. 6.4e+03;

```



Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 DMT 8

|||

Db 6 DMT 8

#### RESULT 5

US-09-935-682-56

; Sequence 56, Application US/09935682

; Patent No. US20020059032A1

; GENERAL INFORMATION:

; APPLICANT: Societe de Conseils de Recherches et D'Applications Scientifiques

; APPLICANT: Ferrer, Camara Y.

; TITLE OF INVENTION: Rational Selection of Putative Peptides from Identified Nucleotide or

; TITLE OF INVENTION: Peptide Sequences

; FILE REFERENCE: 58767.000005

; CURRENT APPLICATION NUMBER: US/09/935,682

; CURRENT FILING DATE: 2001-08-24

; PRIOR APPLICATION NUMBER: 09/257,525

; PRIOR FILING DATE: 1999-02-25

; PRIOR APPLICATION NUMBER: PCT/FR00/00460

; PRIOR FILING DATE: 2000-02-24

; NUMBER OF SEQ ID NOS: 73

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 56

; LENGTH: 11

; TYPE: PRT

; ORGANISM: Homo sapiens

US-09-935-682-56

Query Match 27.3%; Score 3; DB 9; Length 11;

Best Local Similarity 100.0%; Pred. No. 6.4e+03;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 TAI 10

|||

Db 9 TAI 11

#### RESULT 6

US-09-813-653-22

; Sequence 22, Application US/09813653

; Patent No. US20020064770A1

; GENERAL INFORMATION:

; APPLICANT: Nestor, John

; APPLICANT: Wilson, Carol

; APPLICANT: See, Raymond

; APPLICANT: Tan Hehir, Christina

; TITLE OF INVENTION: Binding Compounds and Methods For Identifying Binding Compounds

; FILE REFERENCE: CNS-005

; CURRENT APPLICATION NUMBER: US/09/813,653

; CURRENT FILING DATE: 2001-03-20

; PRIOR APPLICATION NUMBER: US 60/190,946

; PRIOR FILING DATE: 2000-03-21

; PRIOR APPLICATION NUMBER: US 60/190,996  
; PRIOR FILING DATE: 2000-03-21  
; PRIOR APPLICATION NUMBER: US 60/191,299  
; PRIOR FILING DATE: 2000-03-21  
; NUMBER OF SEQ ID NOS: 44  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 22  
; LENGTH: 11  
; TYPE: PRT  
; ORGANISM: Artificial sequence  
; FEATURE:  
; OTHER INFORMATION: CPI-10070  
US-09-813-653-22

Query Match 27.3%; Score 3; DB 9; Length 11;  
Best Local Similarity 100.0%; Pred. No. 6.4e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 SRD 6  
|||  
Db 5 SRD 7

RESULT 7

US-09-817-661-19

; Sequence 19, Application US/09817661  
; Patent No. US20020076692A1  
; GENERAL INFORMATION:  
; APPLICANT: Osbourn, Jane  
; APPLICANT: Holet, Thor  
; TITLE OF INVENTION: Improvements to ribosome display  
; FILE REFERENCE: 84633  
; CURRENT APPLICATION NUMBER: US/09/817,661  
; CURRENT FILING DATE: 2001-03-26  
; PRIOR APPLICATION NUMBER: US 60/193,802  
; PRIOR FILING DATE: 2000-03-31  
; NUMBER OF SEQ ID NOS: 35  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 19  
; LENGTH: 11  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-817-661-19

Query Match 27.3%; Score 3; DB 9; Length 11;  
Best Local Similarity 100.0%; Pred. No. 6.4e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 SRD 6  
|||  
Db 2 SRD 4

RESULT 8

US-09-873-676-4

; Sequence 4, Application US/09873676  
; Patent No. US20020077289A1

```
; GENERAL INFORMATION:
; APPLICANT: MacDonald, Nicholas J.
; APPLICANT: Sim, Kim L.
; TITLE OF INVENTION: Angiostatin and Endostatin Binding Proteins and Methods
of Use
; FILE REFERENCE: 05213-0378 (43170-259333)
; CURRENT APPLICATION NUMBER: US/09/873,676
; CURRENT FILING DATE: 2001-06-04
; PRIOR APPLICATION NUMBER: US 60/209,065
; PRIOR FILING DATE: 2000-06-02
; PRIOR APPLICATION NUMBER: US 60/289,387
; PRIOR FILING DATE: 2001-05-08
; NUMBER OF SEQ ID NOS: 123
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic binding peptide
US-09-873-676-4
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Query Match          27.3%; Score 3; DB 9; Length 11;
Best Local Similarity 100.0%; Pred. No. 6.4e+03;
Matches      3; Conservative    0; Mismatches    0; Indels      0; Gaps      0;
```

```
Qy          9 AIK 11
            |||
Db          5 AIK 7
```

# RESULT 9

```
US-09-810-873-2
; Sequence 2, Application US/09810873
; Patent No. US20020106383A1
; GENERAL INFORMATION:
; APPLICANT: Mandrell, David
; APPLICANT: Bates, Anna
; APPLICANT: Brandon, David
; TITLE OF INVENTION: Monoclonal Antibodies Against Campylobacter jejuni and
Campylobacter coli
; TITLE OF INVENTION: Outer Membrane Antigens
; FILE REFERENCE: Mandrell
; CURRENT APPLICATION NUMBER: US/09/810,873
; CURRENT FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 09/277,599
; PRIOR FILING DATE: 1999-03-26
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Campylobacter jejuni
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: ()..()
; OTHER INFORMATION: The undetermined amino acid may or may not exist
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US-09-810-873-2

Query Match 27.3%; Score 3; DB 9; Length 11;  
Best Local Similarity 100.0%; Pred. No. 6.4e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 AIK 11  
|||  
Db 7 AIK 9

RESULT 10

US-09-758-128-25

; Sequence 25, Application US/09758128  
; Patent No. US20020107187A1  
; GENERAL INFORMATION:  
; APPLICANT: KINGSTON, David J.  
; APPLICANT: GERRATY, No. US20020107187Alman L.  
; APPLICANT: WESTBROOK, Simon L.  
; TITLE OF INVENTION: MODULATING THE ACTIVITY OF HORMONES OR THEIR RECEPTORS  
; TITLE OF INVENTION: - PEPTIDES, ANTIBODIES, VACCINES AND USES THEREOF  
; FILE REFERENCE: 016786/0214  
; CURRENT APPLICATION NUMBER: US/09/758,128  
; CURRENT FILING DATE: 2001-01-12  
; PRIOR APPLICATION NUMBER: 09/194,218  
; PRIOR FILING DATE: 1999-02-05  
; PRIOR APPLICATION NUMBER: AU PN9990  
; PRIOR FILING DATE: 1996-05-22  
; NUMBER OF SEQ ID NOS: 58  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 25  
; LENGTH: 11  
; TYPE: PRT  
; ORGANISM: Mouse  
US-09-758-128-25

Query Match 27.3%; Score 3; DB 9; Length 11;  
Best Local Similarity 100.0%; Pred. No. 6.4e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 DMT 8  
|||  
Db 7 DMT 9

RESULT 11

US-09-758-128-28

; Sequence 28, Application US/09758128  
; Patent No. US20020107187A1  
; GENERAL INFORMATION:  
; APPLICANT: KINGSTON, David J.  
; APPLICANT: GERRATY, No. US20020107187Alman L.  
; APPLICANT: WESTBROOK, Simon L.  
; TITLE OF INVENTION: MODULATING THE ACTIVITY OF HORMONES OR THEIR RECEPTORS  
; TITLE OF INVENTION: - PEPTIDES, ANTIBODIES, VACCINES AND USES THEREOF  
; FILE REFERENCE: 016786/0214  
; CURRENT APPLICATION NUMBER: US/09/758,128

; CURRENT FILING DATE: 2001-01-12  
; PRIOR APPLICATION NUMBER: 09/194,218  
; PRIOR FILING DATE: 1999-02-05  
; PRIOR APPLICATION NUMBER: AU PN9990  
; PRIOR FILING DATE: 1996-05-22  
; NUMBER OF SEQ ID NOS: 58  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 28  
; LENGTH: 11  
; TYPE: PRT  
; ORGANISM: Rat  
US-09-758-128-28

Query Match 27.3%; Score 3; DB 9; Length 11;  
Best Local Similarity 100.0%; Pred. No. 6.4e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 DMT 8  
|||  
Db 7 DMT 9

RESULT 12

US-09-949-196-16

; Sequence 16, Application US/09949196  
; Patent No. US20020147145A1  
; GENERAL INFORMATION:  
; APPLICANT: Zealand Pharmaceuticals A/S  
; TITLE OF INVENTION: MATERIALS AND METHODS RELATING TO THE DEGRADATION OF  
Cdc25A IN RESPONSE  
; TITLE OF INVENTION: TO DNA DAMAGE  
; FILE REFERENCE: 55888 (45487)  
; CURRENT APPLICATION NUMBER: US/09/949,196  
; CURRENT FILING DATE: 2001-07-09  
; NUMBER OF SEQ ID NOS: 45  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 16  
; LENGTH: 11  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: synthetic peptide  
sequence  
US-09-949-196-16

Query Match 27.3%; Score 3; DB 9; Length 11;  
Best Local Similarity 100.0%; Pred. No. 6.4e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ARK 3  
|||  
Db 2 ARK 4

RESULT 13

US-09-071-838-212

; Sequence 212, Application US/09071838

```

; Patent No. US20020152501A1
; GENERAL INFORMATION:
; APPLICANT: Fischer, Robert L.
; APPLICANT: Ohad, Nir
; APPLICANT: Kiyosue, Tomohiro
; APPLICANT: Yadegari, Ramin
; APPLICANT: Margossian, Linda
; APPLICANT: Harada, John
; APPLICANT: Goldberg, Robert B.
; TITLE OF INVENTION: Nucleic Acids That Control Seed and
; TITLE OF INVENTION: Fruit Development in Plants
; NUMBER OF SEQUENCES: 324
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/071,838
; FILING DATE: 01-MAY-1998
; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: Bastian, Kevin L.
; REGISTRATION NUMBER: 34,774
; REFERENCE/DOCKET NUMBER: 023070-086100US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 212:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-09-071-838-212

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Query Match          27.3%; Score 3; DB 9; Length 11;
Best Local Similarity 100.0%; Pred. No. 6.4e+03;
Matches      3; Conservative      0; Mismatches      0; Indels      0; Gaps      0;

```

```

Qy      2 RKS 4
      |||
Db      2 RKS 4

```

```

RESULT 14
US-09-758-426-25
; Sequence 25, Application US/09758426
; Patent No. US20020169116A1
; GENERAL INFORMATION:

```

```
; APPLICANT: KINGSTON, David J.
; APPLICANT: GERRATY, No. US20020169116Alman L.
; APPLICANT: WESTBROOK, Simon L.
; TITLE OF INVENTION: MODULATING THE ACTIVITY OF HORMONES OR THEIR RECEPTORS
; TITLE OF INVENTION: - PEPTIDES, ANTIBODIES, VACCINES AND USES THEREOF
; FILE REFERENCE: 016786/0214
; CURRENT APPLICATION NUMBER: US/09/758,426
; CURRENT FILING DATE: 2001-01-12
; PRIOR APPLICATION NUMBER: 09/194,218
; PRIOR FILING DATE: 1999-02-05
; PRIOR APPLICATION NUMBER: AU PN9990
; PRIOR FILING DATE: 1996-05-22
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 25
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Mouse
US-09-758-426-25
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Query Match          27.3%; Score 3; DB 9; Length 11;
Best Local Similarity 100.0%; Pred. No. 6.4e+03;
Matches      3; Conservative      0; Mismatches      0; Indels      0; Gaps      0;
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Qy          6 DMT 8
            |||
Db          7 DMT 9
```

# RESULT 15

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US-09-758-426-28
; Sequence 28, Application US/09758426
; Patent No. US20020169116Al
; GENERAL INFORMATION:
; APPLICANT: KINGSTON, David J.
; APPLICANT: GERRATY, No. US20020169116Alman L.
; APPLICANT: WESTBROOK, Simon L.
; TITLE OF INVENTION: MODULATING THE ACTIVITY OF HORMONES OR THEIR RECEPTORS
; TITLE OF INVENTION: - PEPTIDES, ANTIBODIES, VACCINES AND USES THEREOF
; FILE REFERENCE: 016786/0214
; CURRENT APPLICATION NUMBER: US/09/758,426
; CURRENT FILING DATE: 2001-01-12
; PRIOR APPLICATION NUMBER: 09/194,218
; PRIOR FILING DATE: 1999-02-05
; PRIOR APPLICATION NUMBER: AU PN9990
; PRIOR FILING DATE: 1996-05-22
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 28
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Rat
US-09-758-426-28
```

```
Query Match          27.3%; Score 3; DB 9; Length 11;
Best Local Similarity 100.0%; Pred. No. 6.4e+03;
Matches      3; Conservative      0; Mismatches      0; Indels      0; Gaps      0;
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Qy 6 DMT 8  
|||  
Db 7 DMT 9

RESULT 16

US-09-758-198-25

; Sequence 25, Application US/09758198  
; Publication No. US20020187925A1  
; GENERAL INFORMATION:  
; APPLICANT: KINGSTON, David J.  
; APPLICANT: GERRATY, No. US20020187925A1man L.  
; APPLICANT: WESTBROOK, Simon L.  
; TITLE OF INVENTION: MODULATING THE ACTIVITY OF HORMONES OR THEIR RECEPTORS  
; TITLE OF INVENTION: - PEPTIDES, ANTIBODIES, VACCINES AND USES THEREOF  
; FILE REFERENCE: 016786/0214  
; CURRENT APPLICATION NUMBER: US/09/758,198  
; CURRENT FILING DATE: 2001-01-12  
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US/09/194,218  
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-02-05  
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: PCT/AU97/00312  
; PRIOR FILING DATE: EARLIER FILING DATE: 1997-05-22  
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: AU PN9990  
; PRIOR FILING DATE: EARLIER FILING DATE: 1996-05-22  
; NUMBER OF SEQ ID NOS: 58  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 25  
; LENGTH: 11  
; TYPE: PRT  
; ORGANISM: Mouse  
US-09-758-198-25

Query Match 27.3%; Score 3; DB 9; Length 11;  
Best Local Similarity 100.0%; Pred. No. 6.4e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 DMT 8  
|||  
Db 7 DMT 9

RESULT 17

US-09-758-198-28

; Sequence 28, Application US/09758198  
; Publication No. US20020187925A1  
; GENERAL INFORMATION:  
; APPLICANT: KINGSTON, David J.  
; APPLICANT: GERRATY, No. US20020187925A1man L.  
; APPLICANT: WESTBROOK, Simon L.  
; TITLE OF INVENTION: MODULATING THE ACTIVITY OF HORMONES OR THEIR RECEPTORS  
; TITLE OF INVENTION: - PEPTIDES, ANTIBODIES, VACCINES AND USES THEREOF  
; FILE REFERENCE: 016786/0214  
; CURRENT APPLICATION NUMBER: US/09/758,198  
; CURRENT FILING DATE: 2001-01-12  
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US/09/194,218  
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-02-05



; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: PCT/AU97/00312  
; PRIOR FILING DATE: EARLIER FILING DATE: 1997-05-22  
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: AU PN9990  
; PRIOR FILING DATE: EARLIER FILING DATE: 1996-05-22  
; NUMBER OF SEQ ID NOS: 58  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 28  
; LENGTH: 11  
; TYPE: PRT  
; ORGANISM: Rat  
US-09-758-198-28

Query Match 27.3%; Score 3; DB 9; Length 11;  
Best Local Similarity 100.0%; Pred. No. 6.4e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 DMT 8  
|||  
Db 7 DMT 9

RESULT 18

US-09-983-802-567

; Sequence 567, Application US/09983802  
; Publication No. US20030022185A1  
; GENERAL INFORMATION:  
; APPLICANT: Fischer et al.  
; TITLE OF INVENTION: 123 Human Secreted Proteins  
; FILE REFERENCE: PZ010P1  
; CURRENT APPLICATION NUMBER: US/09/983,802  
; CURRENT FILING DATE: 2001-10-25  
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/227,357  
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-01-08  
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: PCT/US98/13684  
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-07-07  
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/051,926  
; PRIOR FILING DATE: EARLIER FILING DATE: 1997-07-08  
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/052,793  
; PRIOR FILING DATE: EARLIER FILING DATE: 1997-07-08  
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/051,925  
; PRIOR FILING DATE: EARLIER FILING DATE: 1997-07-08  
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/051,929  
; PRIOR FILING DATE: EARLIER FILING DATE: 1997-07-08  
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/052,803  
; PRIOR FILING DATE: EARLIER FILING DATE: 1997-07-08  
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/052,732  
; PRIOR FILING DATE: EARLIER FILING DATE: 1997-07-08  
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/051,931  
; PRIOR FILING DATE: EARLIER FILING DATE: 1997-07-08  
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/051,932  
; PRIOR FILING DATE: EARLIER FILING DATE: 1997-07-08  
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/051,916  
; PRIOR FILING DATE: EARLIER FILING DATE: 1997-07-08  
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/051,930  
; PRIOR FILING DATE: EARLIER FILING DATE: 1997-07-08  
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/051,918  
; PRIOR FILING DATE: EARLIER FILING DATE: 1997-07-08

```

; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/051,920
; PRIOR FILING DATE: EARLIER FILING DATE: 1997-07-08
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/052,733
; PRIOR FILING DATE: EARLIER FILING DATE: 1997-07-08
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/052,795
; PRIOR FILING DATE: EARLIER FILING DATE: 1997-07-08
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/051,919
; PRIOR FILING DATE: EARLIER FILING DATE: 1997-07-08
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/051,928
; PRIOR FILING DATE: EARLIER FILING DATE: 1997-07-08
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/055,722
; PRIOR FILING DATE: EARLIER FILING DATE: 1997-08-18
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/055,723
; PRIOR FILING DATE: EARLIER FILING DATE: 1997-08-18
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/055,948
; PRIOR FILING DATE: EARLIER FILING DATE: 1997-08-18
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/055,949
; PRIOR FILING DATE: EARLIER FILING DATE: 1997-08-18
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/055,953
; PRIOR FILING DATE: EARLIER FILING DATE: 1997-08-18
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/055,950
; PRIOR FILING DATE: EARLIER FILING DATE: 1997-08-18
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/055,947
; PRIOR FILING DATE: EARLIER FILING DATE: 1997-08-18
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/055,964
; PRIOR FILING DATE: EARLIER FILING DATE: 1997-08-18
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/056,360
; PRIOR FILING DATE: EARLIER FILING DATE: 1997-08-18
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/055,684
; PRIOR FILING DATE: EARLIER FILING DATE: 1997-08-18
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/055,984
; PRIOR FILING DATE: EARLIER FILING DATE: 1997-08-18
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/055,954
; PRIOR FILING DATE: EARLIER FILING DATE: 1997-08-18
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/058,785
; PRIOR FILING DATE: EARLIER FILING DATE: 1997-09-12
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/058,664
; PRIOR FILING DATE: EARLIER FILING DATE: 1997-09-12
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/058,660
; PRIOR FILING DATE: EARLIER FILING DATE: 1997-09-12
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/058,661
; PRIOR FILING DATE: EARLIER FILING DATE: 1997-09-12
; NUMBER OF SEQ ID NOS: 672
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 567
;   LENGTH: 11
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-983-802-567

```

```

Query Match          27.3%; Score 3; DB 10; Length 11;
Best Local Similarity 100.0%; Pred. No. 6.4e+03;
Matches      3; Conservative      0; Mismatches      0; Indels      0; Gaps      0;

```

```

Qy          9 AIK 11
            |||
Db          7 AIK 9

```

RESULT 19

US-09-882-291-44

```
; Sequence 44, Application US/09882291
; Publication No. US20030040472A1
; GENERAL INFORMATION:
; APPLICANT: Zealand Pharmaceuticals A/S
; TITLE OF INVENTION: No. US20030040472A1e1 Peptide Conjugates
; FILE REFERENCE: 007-2001
; CURRENT APPLICATION NUMBER: US/09/882,291
; CURRENT FILING DATE: 2001-06-15
; NUMBER OF SEQ ID NOS: 77
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 44
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic peptide
sequence
US-09-882-291-44
```

```
Query Match          27.3%; Score 3; DB 10; Length 11;
Best Local Similarity 100.0%; Pred. No. 6.4e+03;
Matches      3; Conservative      0; Mismatches      0; Indels      0; Gaps      0;
```

```
Qy      1 ARK 3
        |||
Db      2 ARK 4
```

RESULT 20

US-09-861-661-25

```
; Sequence 25, Application US/09861661
; Publication No. US20030045676A1
; GENERAL INFORMATION:
; APPLICANT: KINGSTON, DAVID J.
; APPLICANT: GERRATY, NORMAN L.
; APPLICANT: WESTBROOK, SIMON L.
; TITLE OF INVENTION: PEPTIDES, ANTIBODIES, VACCINES & USES THEREOF
; FILE REFERENCE: 054270/0135
; CURRENT APPLICATION NUMBER: US/09/861,661
; CURRENT FILING DATE: 2001-05-22
; PRIOR APPLICATION NUMBER: 09/194,218
; PRIOR FILING DATE: 1999-02-05
; PRIOR APPLICATION NUMBER: AU PN9990
; PRIOR FILING DATE: 1996-05-22
; NUMBER OF SEQ ID NOS: 59
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 25
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Mus sp.
US-09-861-661-25
```

```
Query Match          27.3%; Score 3; DB 10; Length 11;
```

Best Local Similarity 100.0%; Pred. No. 6.4e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 DMT 8  
|||  
Db 7 DMT 9

RESULT 21

US-09-861-661-28

; Sequence 28, Application US/09861661  
; Publication No. US20030045676A1  
; GENERAL INFORMATION:  
; APPLICANT: KINGSTON, DAVID J.  
; APPLICANT: GERRATY, NORMAN L.  
; APPLICANT: WESTBROOK, SIMON L.  
; TITLE OF INVENTION: PEPTIDES, ANTIBODIES, VACCINES & USES THEREOF  
; FILE REFERENCE: 054270/0135  
; CURRENT APPLICATION NUMBER: US/09/861,661  
; CURRENT FILING DATE: 2001-05-22  
; PRIOR APPLICATION NUMBER: 09/194,218  
; PRIOR FILING DATE: 1999-02-05  
; PRIOR APPLICATION NUMBER: AU PN9990  
; PRIOR FILING DATE: 1996-05-22  
; NUMBER OF SEQ ID NOS: 59  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 28  
; LENGTH: 11  
; TYPE: PRT  
; ORGANISM: Rattus sp.  
US-09-861-661-28

Query Match 27.3%; Score 3; DB 10; Length 11;  
Best Local Similarity 100.0%; Pred. No. 6.4e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 DMT 8  
|||  
Db 7 DMT 9

RESULT 22

US-09-809-391-698

; Sequence 698, Application US/09809391  
; Publication No. US20030049618A1  
; GENERAL INFORMATION:  
; APPLICANT: Ruben et al.  
; TITLE OF INVENTION: 186 Human Secreted proteins  
; FILE REFERENCE: PZ002P2  
; CURRENT APPLICATION NUMBER: US/09/809,391  
; CURRENT FILING DATE: 2001-03-16  
; Prior application data removed - consult PALM or file wrapper  
; NUMBER OF SEQ ID NOS: 761  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 698  
; LENGTH: 11  
; TYPE: PRT

; ORGANISM: Homo sapiens  
US-09-809-391-698

Query Match 27.3%; Score 3; DB 10; Length 11;  
Best Local Similarity 100.0%; Pred. No. 6.4e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 AIK 11  
|||  
Db 4 AIK 6

RESULT 23

US-09-775-052-3

; Sequence 3, Application US/09775052  
; Publication No. US20030054000A1  
; GENERAL INFORMATION:  
; APPLICANT: Dowdy, Steven F.  
; TITLE OF INVENTION: ANTI-PATHOGEN SYSTEM AND METHODS OF USE THEREOF  
; FILE REFERENCE: 48881/1742  
; CURRENT APPLICATION NUMBER: US/09/775,052  
; CURRENT FILING DATE: 2001-02-01  
; PRIOR APPLICATION NUMBER: 09/208,966  
; PRIOR FILING DATE: 1998-12-10  
; PRIOR APPLICATION NUMBER: 60/082,402  
; PRIOR FILING DATE: 1998-04-20  
; PRIOR APPLICATION NUMBER: 60/069,012  
; PRIOR FILING DATE: 1997-12-10  
; NUMBER OF SEQ ID NOS: 57  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 3  
; LENGTH: 11  
; TYPE: PRT  
; ORGANISM: human  
US-09-775-052-3

Query Match 27.3%; Score 3; DB 10; Length 11;  
Best Local Similarity 100.0%; Pred. No. 6.4e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ARK 3  
|||  
Db 2 ARK 4

RESULT 24

US-09-847-946A-126

; Sequence 126, Application US/09847946A  
; Publication No. US20030054999A1  
; GENERAL INFORMATION:  
; APPLICANT: May, Michael J  
; APPLICANT: Ghosh, Sankar  
; APPLICANT: Findeis, Mark A  
; APPLICANT: Phillips, Kathryn  
; APPLICANT: Hannig, Gerhard  
; TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF  
; FILE REFERENCE: PPI-119

```

; CURRENT APPLICATION NUMBER: US/09/847,946A
; CURRENT FILING DATE: 2001-05-02
; PRIOR APPLICATION NUMBER: 60/201,261
; PRIOR FILING DATE: 2000-05-02
; PRIOR APPLICATION NUMBER: 09/643,260
; PRIOR FILING DATE: 2000-08-22
; NUMBER OF SEQ ID NOS: 160
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 126
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:membrane
; OTHER INFORMATION: translocation domain
US-09-847-946A-126

```

```

Query Match          27.3%; Score 3; DB 10; Length 11;
Best Local Similarity 100.0%; Pred. No. 6.4e+03;
Matches      3; Conservative    0; Mismatches    0; Indels      0; Gaps      0;

```

```

Qy          1 ARK 3
            |||
Db          2 ARK 4

```

# RESULT 25

```

US-09-847-946A-127
; Sequence 127, Application US/09847946A
; Publication No. US20030054999A1
; GENERAL INFORMATION:
; APPLICANT: May, Michael J
; APPLICANT: Ghosh, Sankar
; APPLICANT: Findeis, Mark A
; APPLICANT: Phillips, Kathryn
; APPLICANT: Hannig, Gerhard
; TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF
; FILE REFERENCE: PPI-119
; CURRENT APPLICATION NUMBER: US/09/847,946A
; CURRENT FILING DATE: 2001-05-02
; PRIOR APPLICATION NUMBER: 60/201,261
; PRIOR FILING DATE: 2000-05-02
; PRIOR APPLICATION NUMBER: 09/643,260
; PRIOR FILING DATE: 2000-08-22
; NUMBER OF SEQ ID NOS: 160
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 127
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:membrane
; OTHER INFORMATION: translocation domain
US-09-847-946A-127

```

```

Query Match          27.3%; Score 3; DB 10; Length 11;
Best Local Similarity 100.0%; Pred. No. 6.4e+03;

```

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ARK 3  
|||  
Db 2 ARK 4

RESULT 26

US-09-880-748-3177

; Sequence 3177, Application US/09880748  
; Publication No. US20030059937A1  
; GENERAL INFORMATION:  
; APPLICANT: Ruben et al.  
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind BLyS  
; FILE REFERENCE: PF523  
; CURRENT APPLICATION NUMBER: US/09/880,748  
; CURRENT FILING DATE: 2001-06-15  
; PRIOR APPLICATION NUMBER: 60/212,210  
; PRIOR FILING DATE: 2000-06-15  
; PRIOR APPLICATION NUMBER: 60/240,816  
; PRIOR FILING DATE: 2000-10-17  
; PRIOR APPLICATION NUMBER: 60/276,248  
; PRIOR FILING DATE: 2001-03-16  
; PRIOR APPLICATION NUMBER: 60/277,379  
; PRIOR FILING DATE: 2001-03-21  
; PRIOR APPLICATION NUMBER: 60/293,499  
; PRIOR FILING DATE: 2001-05-25  
; NUMBER OF SEQ ID NOS: 3239  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 3177  
; LENGTH: 11  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-880-748-3177

Query Match 27.3%; Score 3; DB 10; Length 11;

Best Local Similarity 100.0%; Pred. No. 6.4e+03;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 DMT 8  
|||  
Db 3 DMT 5

RESULT 27

US-09-876-904A-33

; Sequence 33, Application US/09876904A  
; Publication No. US20030072794A1  
; GENERAL INFORMATION:  
; APPLICANT: BOULIKAS, TENI  
; TITLE OF INVENTION: ENCAPSULATION OF PLASMID DNA (LIPOGENES TM) AND  
THERAPEUTIC  
; TITLE OF INVENTION: AGENTS WITH NUCLEAR LOCALIZATION SIGNAL/FUSOGENIC  
PEPTIDE  
; TITLE OF INVENTION: CONJUGATES INTO TARGETED LIPOSOME COMPLEXES  
; FILE REFERENCE: TB-2002.00  
; CURRENT APPLICATION NUMBER: US/09/876,904A

```

; CURRENT FILING DATE: 2001-06-08
; PRIOR APPLICATION NUMBER: US 60/210,925
; PRIOR FILING DATE: 2000-06-09
; NUMBER OF SEQ ID NOS: 629
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 33
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic Polymavirus
; OTHER INFORMATION: major capsid protein VP1
US-09-876-904A-33

```

```

Query Match          27.3%; Score 3; DB 10; Length 11;
Best Local Similarity 100.0%; Pred. No. 6.4e+03;
Matches      3; Conservative      0; Mismatches      0; Indels      0; Gaps      0;

```

```

Qy      2 RKS 4
      |||
Db      4 RKS 6

```

# RESULT 28

```

US-09-876-904A-236
; Sequence 236, Application US/09876904A
; Publication No. US20030072794A1
; GENERAL INFORMATION:
; APPLICANT: BOULIKAS, TENI
; TITLE OF INVENTION: ENCAPSULATION OF PLASMID DNA (LIPOGENES TM) AND THERAPEUTIC
; TITLE OF INVENTION: AGENTS WITH NUCLEAR LOCALIZATION SIGNAL/FUSOGENIC PEPTIDE
; TITLE OF INVENTION: CONJUGATES INTO TARGETED LIPOSOME COMPLEXES
; FILE REFERENCE: TB-2002.00
; CURRENT APPLICATION NUMBER: US/09/876,904A
; CURRENT FILING DATE: 2001-06-08
; PRIOR APPLICATION NUMBER: US 60/210,925
; PRIOR FILING DATE: 2000-06-09
; NUMBER OF SEQ ID NOS: 629
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 236
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Unknown Organism
; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism: Hydrophilic protein
US-09-876-904A-236

```

```

Query Match          27.3%; Score 3; DB 10; Length 11;
Best Local Similarity 100.0%; Pred. No. 6.4e+03;
Matches      3; Conservative      0; Mismatches      0; Indels      0; Gaps      0;

```

```

Qy      1 ARK 3
      |||
Db      7 ARK 9

```



RESULT 29

US-09-876-904A-509

; Sequence 509, Application US/09876904A

; Publication No. US20030072794A1

; GENERAL INFORMATION:

; APPLICANT: BOULIKAS, TENI

; TITLE OF INVENTION: ENCAPSULATION OF PLASMID DNA (LIPOGENES TM) AND THERAPEUTIC

; TITLE OF INVENTION: AGENTS WITH NUCLEAR LOCALIZATION SIGNAL/FUSOGENIC PEPTIDE

; TITLE OF INVENTION: CONJUGATES INTO TARGETED LIPOSOME COMPLEXES

; FILE REFERENCE: TB-2002.00

; CURRENT APPLICATION NUMBER: US/09/876,904A

; CURRENT FILING DATE: 2001-06-08

; PRIOR APPLICATION NUMBER: US 60/210,925

; PRIOR FILING DATE: 2000-06-09

; NUMBER OF SEQ ID NOS: 629

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 509

; LENGTH: 11

; TYPE: PRT

; ORGANISM: Unknown Organism

; FEATURE:

; OTHER INFORMATION: Description of Unknown Organism: Ig/EBP-1 (immunoglobulin

; OTHER INFORMATION: gene enhancer-binding protein).

US-09-876-904A-509

Query Match 27.3%; Score 3; DB 10; Length 11;

Best Local Similarity 100.0%; Pred. No. 6.4e+03;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 KSR 5

|||

Db 3 KSR 5

RESULT 30

US-09-972-656-6

; Sequence 6, Application US/09972656

; Publication No. US20030099647A1

; GENERAL INFORMATION:

; APPLICANT: Deshpande, Rajendra

; APPLICANT: Tsai, Mei-Mei

; TITLE OF INVENTION: Fully Human Antibody Fab Fragments with Human Interferon-Gamma

; TITLE OF INVENTION: Neutralizing Activity

; FILE REFERENCE: A-799

; CURRENT APPLICATION NUMBER: US/09/972,656

; CURRENT FILING DATE: 2001-10-05

; NUMBER OF SEQ ID NOS: 135

; SOFTWARE: PatentIn version 3.0

; SEQ ID NO 6

; LENGTH: 11

; TYPE: PRT

; ORGANISM: Homo sapiens

US-09-972-656-6

Query Match 27.3%; Score 3; DB 10; Length 11;  
Best Local Similarity 100.0%; Pred. No. 6.4e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ARK 3  
|||  
Db 6 ARK 8

RESULT 31

US-09-802-083-10

; Sequence 10, Application US/09802083  
; Publication No. US20030119075A1  
; GENERAL INFORMATION:  
; APPLICANT: Kirchhofer, Daniel K.  
; APPLICANT: Lowe, David G.  
; APPLICANT: Presta, Leonard G.  
; TITLE OF INVENTION: Anti-Tissue Factor Antibodies with Enhanced  
; TITLE OF INVENTION: Anticoagulant Potency  
; FILE REFERENCE: P1736R1  
; CURRENT APPLICATION NUMBER: US/09/802,083  
; CURRENT FILING DATE: 2001-03-08  
; PRIOR APPLICATION NUMBER: US 60/189,775  
; PRIOR FILING DATE: 2000-03-16  
; NUMBER OF SEQ ID NOS: 28  
; SEQ ID NO 10  
; LENGTH: 11  
; TYPE: PRT  
; ORGANISM: Mus musculus  
US-09-802-083-10

Query Match 27.3%; Score 3; DB 10; Length 11;  
Best Local Similarity 100.0%; Pred. No. 6.4e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 SRD 6  
|||  
Db 3 SRD 5

RESULT 32

US-09-882-171-698

; Sequence 698, Application US/09882171  
; Publication No. US20030175858A1  
; GENERAL INFORMATION:  
; APPLICANT: Ruben et al.  
; TITLE OF INVENTION: 186 Human Secreted proteins  
; FILE REFERENCE: PZ002P2  
; CURRENT APPLICATION NUMBER: US/09/882,171  
; CURRENT FILING DATE: 2001-06-18  
; PRIOR APPLICATION NUMBER: 09/809,391  
; PRIOR FILING DATE: 2001-03-16  
; PRIOR APPLICATION NUMBER: 09/149,476  
; PRIOR FILING DATE: 1998-09-08  
; PRIOR APPLICATION NUMBER: PCT/US98/04493

; PRIOR FILING DATE: 1998-03-06  
; PRIOR APPLICATION NUMBER: 60/040,162  
; PRIOR FILING DATE: 1997-03-07  
; PRIOR APPLICATION NUMBER: 60/040,333  
; PRIOR FILING DATE: 1997-03-07  
; PRIOR APPLICATION NUMBER: 60/038,621  
; PRIOR FILING DATE: 1997-03-07  
; PRIOR APPLICATION NUMBER: 60/040,626  
; PRIOR FILING DATE: 1997-03-07  
; PRIOR APPLICATION NUMBER: 60/040,334  
; PRIOR FILING DATE: 1997-03-07  
; PRIOR APPLICATION NUMBER: 60/040,336  
; PRIOR FILING DATE: 1997-03-07  
; PRIOR APPLICATION NUMBER: 60/040,163  
; PRIOR FILING DATE: 1997-03-07  
; PRIOR APPLICATION NUMBER: 60/047,600  
; PRIOR FILING DATE: 1997-05-23  
; PRIOR APPLICATION NUMBER: 60/047,615  
; PRIOR FILING DATE: 1997-05-23  
; PRIOR APPLICATION NUMBER: 60/047,597  
; PRIOR FILING DATE: 1997-05-23  
; PRIOR APPLICATION NUMBER: 60/047,502  
; PRIOR FILING DATE: 1997-05-23  
; PRIOR APPLICATION NUMBER: 60/047,633  
; PRIOR FILING DATE: 1997-05-23  
; PRIOR APPLICATION NUMBER: 60/047,583  
; PRIOR FILING DATE: 1997-05-23  
; PRIOR APPLICATION NUMBER: 60/047,617  
; PRIOR FILING DATE: 1997-05-23  
; PRIOR APPLICATION NUMBER: 60/047,618  
; PRIOR FILING DATE: 1997-05-23  
; PRIOR APPLICATION NUMBER: 60/047,503  
; PRIOR FILING DATE: 1997-05-23  
; PRIOR APPLICATION NUMBER: 60/047,592  
; PRIOR FILING DATE: 1997-05-23  
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; PRIOR FILING DATE: 1997-05-23  
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; PRIOR FILING DATE: 1997-05-23  
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; PRIOR FILING DATE: 1997-05-23  
; PRIOR APPLICATION NUMBER: 60/047,587  
; PRIOR FILING DATE: 1997-05-23  
; PRIOR APPLICATION NUMBER: 60/047,492  
; PRIOR FILING DATE: 1997-05-23  
; PRIOR APPLICATION NUMBER: 60/047,598  
; PRIOR FILING DATE: 1997-05-23  
; PRIOR APPLICATION NUMBER: 60/047,613  
; PRIOR FILING DATE: 1997-05-23  
; PRIOR APPLICATION NUMBER: 60/047,582  
; PRIOR FILING DATE: 1997-05-23  
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; PRIOR FILING DATE: 1997-05-23  
; PRIOR APPLICATION NUMBER: 60/047,612  
; PRIOR FILING DATE: 1997-05-23  
; PRIOR APPLICATION NUMBER: 60/047,632  
; PRIOR FILING DATE: 1997-05-23

; PRIOR APPLICATION NUMBER: 60/047,601  
; PRIOR FILING DATE: 1997-05-23  
; PRIOR APPLICATION NUMBER: 60/043,580  
; PRIOR FILING DATE: 1997-04-11  
; PRIOR APPLICATION NUMBER: 60/043,568  
; PRIOR FILING DATE: 1997-04-11  
; PRIOR APPLICATION NUMBER: 60/043,314  
; PRIOR FILING DATE: 1997-04-11  
; PRIOR APPLICATION NUMBER: 60/043,569  
; PRIOR FILING DATE: 1997-04-11  
; PRIOR APPLICATION NUMBER: 60/043,311  
; PRIOR FILING DATE: 1997-04-11  
; PRIOR APPLICATION NUMBER: 60/043,671  
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; PRIOR APPLICATION NUMBER: 60/043,674  
; PRIOR FILING DATE: 1997-04-11  
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; PRIOR FILING DATE: 1997-04-11  
; PRIOR APPLICATION NUMBER: 60/043,672  
; PRIOR FILING DATE: 1997-04-11  
; PRIOR APPLICATION NUMBER: 60/043,315  
; PRIOR FILING DATE: 1997-04-11  
; PRIOR APPLICATION NUMBER: 60/048,974  
; PRIOR FILING DATE: 1997-06-06  
; PRIOR APPLICATION NUMBER: 60/056,886  
; PRIOR FILING DATE: 1997-08-22  
; PRIOR APPLICATION NUMBER: 60/056,877  
; PRIOR FILING DATE: 1997-08-22  
; PRIOR APPLICATION NUMBER: 60/056,889  
; PRIOR FILING DATE: 1997-08-22  
; PRIOR APPLICATION NUMBER: 60/056,893  
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; PRIOR APPLICATION NUMBER: 60/056,662  
; PRIOR FILING DATE: 1997-08-22  
; PRIOR APPLICATION NUMBER: 60/056,872  
; PRIOR FILING DATE: 1997-08-22  
; PRIOR APPLICATION NUMBER: 60/056,882  
; PRIOR FILING DATE: 1997-08-22  
; PRIOR APPLICATION NUMBER: 60/056,637  
; PRIOR FILING DATE: 1997-08-22  
; PRIOR APPLICATION NUMBER: 60/056,903  
; PRIOR FILING DATE: 1997-08-22  
; PRIOR APPLICATION NUMBER: 60/056,888  
; PRIOR FILING DATE: 1997-08-22  
; PRIOR APPLICATION NUMBER: 60/056,879  
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; PRIOR APPLICATION NUMBER: 60/056,880  
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; PRIOR APPLICATION NUMBER: 60/056,894

; PRIOR FILING DATE: 1997-08-22  
; PRIOR APPLICATION NUMBER: 60/056,911  
; PRIOR FILING DATE: 1997-08-22  
; PRIOR APPLICATION NUMBER: 60/056,636  
; PRIOR FILING DATE: 1997-08-22  
; PRIOR APPLICATION NUMBER: 60/056,874  
; PRIOR FILING DATE: 1997-08-22  
; PRIOR APPLICATION NUMBER: 60/056,910  
; PRIOR FILING DATE: 1997-08-22  
; PRIOR APPLICATION NUMBER: 60/056,864  
; PRIOR FILING DATE: 1997-08-22  
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; PRIOR FILING DATE: 1997-08-22  
; PRIOR APPLICATION NUMBER: 60/056,845  
; PRIOR FILING DATE: 1997-08-22  
; PRIOR APPLICATION NUMBER: 60/056,892  
; PRIOR FILING DATE: 1997-08-22  
; PRIOR APPLICATION NUMBER: 60/057,761  
; PRIOR FILING DATE: 1997-08-22  
; PRIOR APPLICATION NUMBER: 60/047,595  
; PRIOR FILING DATE: 1997-05-23  
; PRIOR APPLICATION NUMBER: 60/047,599  
; PRIOR FILING DATE: 1997-05-23  
; PRIOR APPLICATION NUMBER: 60/047,588  
; PRIOR FILING DATE: 1997-05-23  
; PRIOR APPLICATION NUMBER: 60/047,585  
; PRIOR FILING DATE: 1997-05-23  
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; PRIOR FILING DATE: 1997-05-23  
; PRIOR APPLICATION NUMBER: 60/047,590  
; PRIOR FILING DATE: 1997-05-23  
; PRIOR APPLICATION NUMBER: 60/047,594  
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; PRIOR APPLICATION NUMBER: 60/047,589  
; PRIOR FILING DATE: 1997-05-23  
; PRIOR APPLICATION NUMBER: 60/047,593  
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; PRIOR APPLICATION NUMBER: 60/047,614  
; PRIOR FILING DATE: 1997-05-23  
; PRIOR APPLICATION NUMBER: 60/043,578  
; PRIOR FILING DATE: 1997-04-11  
; PRIOR APPLICATION NUMBER: 60/043,576  
; PRIOR FILING DATE: 1997-04-11  
; PRIOR APPLICATION NUMBER: 60/047,501  
; PRIOR FILING DATE: 1997-05-23  
; PRIOR APPLICATION NUMBER: 60/043,670  
; PRIOR FILING DATE: 1997-04-11  
; PRIOR APPLICATION NUMBER: 60/056,632  
; PRIOR FILING DATE: 1997-08-22  
; PRIOR APPLICATION NUMBER: 60/056,664  
; PRIOR FILING DATE: 1997-08-22  
; PRIOR APPLICATION NUMBER: 60/056,876  
; PRIOR FILING DATE: 1997-08-22  
; PRIOR APPLICATION NUMBER: 60/056,881  
; PRIOR FILING DATE: 1997-08-22  
; PRIOR APPLICATION NUMBER: 60/056,909  
; PRIOR FILING DATE: 1997-08-22

; PRIOR APPLICATION NUMBER: 60/056,875  
 ; PRIOR FILING DATE: 1997-08-22  
 ; PRIOR APPLICATION NUMBER: 60/056,862  
 ; PRIOR FILING DATE: 1997-08-22  
 ; PRIOR APPLICATION NUMBER: 60/056,887  
 ; PRIOR FILING DATE: 1997-08-22  
 ; PRIOR APPLICATION NUMBER: 60/056,908  
 ; PRIOR FILING DATE: 1997-08-22  
 ; PRIOR APPLICATION NUMBER: 60/048,964  
 ; PRIOR FILING DATE: 1997-06-06  
 ; PRIOR APPLICATION NUMBER: 60/057,650  
 ; PRIOR FILING DATE: 1997-09-05  
 ; PRIOR APPLICATION NUMBER: 60/056,884  
 ; PRIOR FILING DATE: 1997-08-22  
 ; PRIOR APPLICATION NUMBER: 60/057,669  
 ; PRIOR FILING DATE: 1997-09-05

Query Match 27.3%; Score 3; DB 10; Length 11;  
 Best Local Similarity 100.0%; Pred. No. 6.4e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 AIK 11  
 |||  
 Db 4 AIK 6

# RESULT 33

US-09-973-278-398

; Sequence 398, Application US/09973278  
 ; Publication No. US20040044191A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Fischer et al.  
 ; TITLE OF INVENTION: 123 Human Secreted Proteins  
 ; FILE REFERENCE: PZ010P2  
 ; CURRENT APPLICATION NUMBER: US/09/973,278  
 ; CURRENT FILING DATE: 2001-10-10  
 ; PRIOR APPLICATION NUMBER: 60/239,899  
 ; PRIOR FILING DATE: 2000-10-13  
 ; PRIOR APPLICATION NUMBER: 09/227,357  
 ; PRIOR FILING DATE: 1999-01-08  
 ; PRIOR APPLICATION NUMBER: PCT/US98/13684  
 ; PRIOR FILING DATE: 1998-07-07  
 ; PRIOR APPLICATION NUMBER: 60/051,926  
 ; PRIOR FILING DATE: 1997-07-08  
 ; PRIOR APPLICATION NUMBER: 60/052,793  
 ; PRIOR FILING DATE: 1997-07-08  
 ; PRIOR APPLICATION NUMBER: 60/051,925  
 ; PRIOR FILING DATE: 1997-07-08  
 ; PRIOR APPLICATION NUMBER: 60/051,929  
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 ; PRIOR APPLICATION NUMBER: 60/052,803  
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 ; PRIOR APPLICATION NUMBER: 60/052,732  
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 ; PRIOR APPLICATION NUMBER: 60/051,931  
 ; PRIOR FILING DATE: 1997-07-08  
 ; PRIOR APPLICATION NUMBER: 60/051,932

; PRIOR FILING DATE: 1997-07-08  
; PRIOR APPLICATION NUMBER: 60/051,916  
; PRIOR FILING DATE: 1997-07-08  
; PRIOR APPLICATION NUMBER: 60/051,930  
; PRIOR FILING DATE: 1997-07-08  
; PRIOR APPLICATION NUMBER: 60/051,918  
; PRIOR FILING DATE: 1997-07-08  
; PRIOR APPLICATION NUMBER: 60/051,920  
; PRIOR FILING DATE: 1997-07-08  
; PRIOR APPLICATION NUMBER: 60/052,733  
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; PRIOR FILING DATE: 1997-07-08  
; PRIOR APPLICATION NUMBER: 60/051,928  
; PRIOR FILING DATE: 1997-07-08  
; PRIOR APPLICATION NUMBER: 60/055,722  
; PRIOR FILING DATE: 1997-08-18  
; PRIOR APPLICATION NUMBER: 60/055,723  
; PRIOR FILING DATE: 1997-08-18  
; PRIOR APPLICATION NUMBER: 60/055,948  
; PRIOR FILING DATE: 1997-08-18  
; PRIOR APPLICATION NUMBER: 60/055,949  
; PRIOR FILING DATE: 1997-08-18  
; PRIOR APPLICATION NUMBER: 60/055,953  
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; PRIOR APPLICATION NUMBER: 60/055,950  
; PRIOR FILING DATE: 1997-08-18  
; PRIOR APPLICATION NUMBER: 60/055,947  
; PRIOR FILING DATE: 1997-08-18  
; PRIOR APPLICATION NUMBER: 60/055,964  
; PRIOR FILING DATE: 1997-08-18  
; PRIOR APPLICATION NUMBER: 60/056,360  
; PRIOR FILING DATE: 1997-08-18  
; PRIOR APPLICATION NUMBER: 60/055,684  
; PRIOR FILING DATE: 1997-08-18  
; PRIOR APPLICATION NUMBER: 60/055,984  
; PRIOR FILING DATE: 1997-08-18  
; PRIOR APPLICATION NUMBER: 60/055,954  
; PRIOR FILING DATE: 1997-08-18  
; PRIOR APPLICATION NUMBER: 60/058,785  
; PRIOR FILING DATE: 1997-09-12  
; PRIOR APPLICATION NUMBER: 60/058,664  
; PRIOR FILING DATE: 1997-09-12  
; PRIOR APPLICATION NUMBER: 60/058,660  
; PRIOR FILING DATE: 1997-09-12  
; PRIOR APPLICATION NUMBER: 60/058,661  
; PRIOR FILING DATE: 1997-09-12  
; NUMBER OF SEQ ID NOS: 947  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 398  
; LENGTH: 11  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-973-278-398

Query Match 27.3%; Score 3; DB 12; Length 11;  
Best Local Similarity 100.0%; Pred. No. 6.4e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 AIK 11  
|||  
Db 7 AIK 9

RESULT 34

US-10-362-527-63

; Sequence 63, Application US/10362527

; Publication No. US20040030106A1

; GENERAL INFORMATION:

; APPLICANT: Friede, Martin

; APPLICANT: Mason, Sean

; APPLICANT: Turnell, William Gordon

; APPLICANT: Vinals Y De Bassols, Carlota

; TITLE OF INVENTION: Vaccine Immunogens Comprising Disulphide Bridged Cyclised Peptide

; TITLE OF INVENTION: and Use Thereof in the Treatment of Allergies

; FILE REFERENCE: B45236

; CURRENT APPLICATION NUMBER: US/10/362,527

; CURRENT FILING DATE: 2003-02-21

; PRIOR APPLICATION NUMBER: PCT/EP01/09576

; PRIOR FILING DATE: 2001-08-17

; PRIOR APPLICATION NUMBER: GB 0020717.5

; PRIOR FILING DATE: 2000-08-22

; NUMBER OF SEQ ID NOS: 328

; SOFTWARE: FastSEQ for Windows Version 4.0

; SEQ ID NO 63

; LENGTH: 11

; TYPE: PRT

; ORGANISM: Homo sapiens

US-10-362-527-63

Query Match 27.3%; Score 3; DB 12; Length 11;  
Best Local Similarity 100.0%; Pred. No. 6.4e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 SRD 6  
|||  
Db 6 SRD 8

RESULT 35

US-10-430-685-39

; Sequence 39, Application US/10430685

; Publication No. US20040039543A1

; GENERAL INFORMATION:

; APPLICANT: KECK, Peter

; TITLE OF INVENTION: COMPUTER METHOD AND APPARATUS FOR CLASSIFYING OBJECTS

; FILE REFERENCE: 63040-010210

; CURRENT APPLICATION NUMBER: US/10/430,685

; CURRENT FILING DATE: 2003-05-06

; PRIOR APPLICATION NUMBER: PCT/US01/44000

; PRIOR FILING DATE: 2001-11-06



; PRIOR APPLICATION NUMBER: 60/246,196  
; PRIOR FILING DATE: 2000-11-06  
; NUMBER OF SEQ ID NOS: 240  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 39  
; LENGTH: 11  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-430-685-39

Query Match 27.3%; Score 3; DB 12; Length 11;  
Best Local Similarity 100.0%; Pred. No. 6.4e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 RKS 4  
|||  
Db 3 RKS 5

RESULT 36

US-10-398-616-4  
; Sequence 4, Application US/10398616  
; Publication No. US20040054143A1  
; GENERAL INFORMATION:  
; APPLICANT: Ark Therapeutics Ltd.  
; TITLE OF INVENTION: VEGF Peptides and Their Use for Inhibiting Angiogenesis  
; FILE REFERENCE: GJE-6525  
; CURRENT APPLICATION NUMBER: US/10/398,616  
; CURRENT FILING DATE: 2003-08-06  
; PRIOR APPLICATION NUMBER: PCT/GB01/04736  
; PRIOR FILING DATE: 2001-10-25  
; NUMBER OF SEQ ID NOS: 21  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 4  
; LENGTH: 11  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Oligopeptide  
US-10-398-616-4

Query Match 27.3%; Score 3; DB 12; Length 11;  
Best Local Similarity 100.0%; Pred. No. 6.4e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 KSR 5  
|||  
Db 7 KSR 9

RESULT 37

US-10-398-616-10  
; Sequence 10, Application US/10398616  
; Publication No. US20040054143A1  
; GENERAL INFORMATION:  
; APPLICANT: Ark Therapeutics Ltd.  
; TITLE OF INVENTION: VEGF Peptides and Their Use for Inhibiting Angiogenesis

; FILE REFERENCE: GJE-6525  
; CURRENT APPLICATION NUMBER: US/10/398,616  
; CURRENT FILING DATE: 2003-08-06  
; PRIOR APPLICATION NUMBER: PCT/GB01/04736  
; PRIOR FILING DATE: 2001-10-25  
; NUMBER OF SEQ ID NOS: 21  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 10  
; LENGTH: 11  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Oligopeptide  
US-10-398-616-10

Query Match 27.3%; Score 3; DB 12; Length 11;  
Best Local Similarity 100.0%; Pred. No. 6.4e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 KSR 5  
|||  
Db 6 KSR 8

RESULT 38

US-09-912-609-27

; Sequence 27, Application US/09912609  
; Publication No. US20020041898A1  
; GENERAL INFORMATION:  
; APPLICANT: UNGER, EVAN C.  
; APPLICANT: MATSUNAGA, TERRY ONICHI  
; APPLICANT: RAMASWAMI, VARADARAJAN  
; APPLICANT: ROMANOWSKI, MAREK J.  
; TITLE OF INVENTION: NOVEL TARGETED DELIVERY SYSTEMS FOR BIOACTIVE AGENTS  
; FILE REFERENCE: 5030-0001.24  
; CURRENT APPLICATION NUMBER: US/09/912,609  
; CURRENT FILING DATE: 2001-07-25  
; PRIOR APPLICATION NUMBER: 09/703,474  
; PRIOR FILING DATE: 2000-10-31  
; PRIOR APPLICATION NUMBER: 09/478,124  
; PRIOR FILING DATE: 2000-01-05  
; NUMBER OF SEQ ID NOS: 131  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 27  
; LENGTH: 11  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
; OTHER INFORMATION: peptide  
US-09-912-609-27

Query Match 27.3%; Score 3; DB 12; Length 11;  
Best Local Similarity 100.0%; Pred. No. 6.4e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 RDM 7

Db                    |||  
                      6 RDM 8

RESULT 39

US-10-060-019-1

; Sequence 1, Application US/10060019  
; Publication No. US20030003564A1  
; GENERAL INFORMATION:  
; APPLICANT: Tyers, Mike  
; APPLICANT: Willems, Andrew  
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR MODULATING UBIQUITIN  
; TITLE OF INVENTION: DEPENDENT PROTEOLYSIS  
; FILE REFERENCE: 11757.10USU1  
; CURRENT APPLICATION NUMBER: US/10/060,019  
; CURRENT FILING DATE: 2002-01-29  
; PRIOR APPLICATION NUMBER: US/09/177,165  
; PRIOR FILING DATE: 1998-10-22  
; PRIOR APPLICATION NUMBER: 60/092,443  
; PRIOR FILING DATE: 1998-07-10  
; PRIOR APPLICATION NUMBER: 60/063,254  
; PRIOR FILING DATE: 1997-10-24  
; NUMBER OF SEQ ID NOS: 50  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 1  
; LENGTH: 11  
; TYPE: PRT  
; ORGANISM: Saccharomyces cerevisiae  
US-10-060-019-1

Query Match                    27.3%; Score 3; DB 14; Length 11;  
Best Local Similarity       100.0%; Pred. No. 6.4e+03;  
Matches       3; Conservative       0; Mismatches       0; Indels       0; Gaps       0;

Qy                    8 TAI 10  
                      |||  
Db                    4 TAI 6

RESULT 40

US-10-211-069-56

; Sequence 56, Application US/10211069  
; Publication No. US20030021797A1  
; GENERAL INFORMATION:  
; APPLICANT: DATTA, Syamal K  
; APPLICANT: KALIYAPERUMAL, Arunan  
; TITLE OF INVENTION: LOCALIZATION OF MAJOR PEPTIDE AUTOEPITOPES FOR NUCLEOSOME  
SPECIF  
; TITLE OF INVENTION: IC T CELLS OF SYSTEMIC LUPUS ERYTHEMATOSUS  
; FILE REFERENCE: 290-13U1 (53662-5017  
; CURRENT APPLICATION NUMBER: US/10/211,069  
; CURRENT FILING DATE: 2002-08-02  
; PRIOR APPLICATION NUMBER: US/09/561,490  
; PRIOR FILING DATE: 2000-04-28  
; PRIOR APPLICATION NUMBER: US 60/131,448  
; PRIOR FILING DATE: 1999-04-28  
; NUMBER OF SEQ ID NOS: 61

; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 56  
; LENGTH: 11  
; TYPE: PRT  
; ORGANISM: Artificial sequence  
; FEATURE:  
; OTHER INFORMATION: Histone fragment  
US-10-211-069-56

Query Match 27.3%; Score 3; DB 14; Length 11;  
Best Local Similarity 100.0%; Pred. No. 6.4e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 KSR 5  
|||  
Db 9 KSR 11

RESULT 41

US-10-062-710-168  
; Sequence 168, Application US/10062710  
; Publication No. US20030049253A1  
; GENERAL INFORMATION:  
; APPLICANT: Li, Frank Q.  
; APPLICANT: Chu, Yong-Liang  
; APPLICANT: Qiu, Jian-Tai  
; TITLE OF INVENTION: Polymeric Conjugates for Delivery of  
; TITLE OF INVENTION: MHC-Recognized Epitopes  
; TITLE OF INVENTION: Via Peptide Vaccines  
; FILE REFERENCE: 3781-001-27  
; CURRENT APPLICATION NUMBER: US/10/062,710  
; CURRENT FILING DATE: 2002-02-05  
; PRIOR APPLICATION NUMBER: US 60/310,498  
; PRIOR FILING DATE: 2001-08-08  
; NUMBER OF SEQ ID NOS: 232  
; SOFTWARE: FastSEQ for Windows Version 4.0  
; SEQ ID NO 168  
; LENGTH: 11  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: HIV B Cell Epitopes  
US-10-062-710-168

Query Match 27.3%; Score 3; DB 14; Length 11;  
Best Local Similarity 100.0%; Pred. No. 6.4e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 SRD 6  
|||  
Db 5 SRD 7

RESULT 42

US-10-229-915-21  
; Sequence 21, Application US/10229915  
; Publication No. US20030083262A1

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; GENERAL INFORMATION:
; APPLICANT: Lazarus, Douglas
; APPLICANT: Hannig, Gerhard
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING INFLAMMATORY
; TITLE OF INVENTION: DISORDERS
; FILE REFERENCE: PPI-127
; CURRENT APPLICATION NUMBER: US/10/229,915
; CURRENT FILING DATE: 2002-08-27
; PRIOR APPLICATION NUMBER: US 60/316,328
; PRIOR FILING DATE: 2001-08-30
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 21
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: anti-inflammatory compound
US-10-229-915-21
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Query Match          27.3%; Score 3; DB 14; Length 11;
Best Local Similarity 100.0%; Pred. No. 6.4e+03;
Matches      3; Conservative      0; Mismatches      0; Indels      0; Gaps      0;
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```
Qy      1 ARK 3
        |||
Db      2 ARK 4
```

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RESULT 43
US-10-227-616-68
; Sequence 68, Application US/10227616
; Publication No. US20030099662A1
; GENERAL INFORMATION:
; APPLICANT: Boyd, Robert Simon
; APPLICANT: Stamps, Alasdair Craig
; APPLICANT: Terrett, Jonathan Alexander
; TITLE OF INVENTION: Proteins
; FILE REFERENCE: 2543-1-028
; CURRENT APPLICATION NUMBER: US/10/227,616
; CURRENT FILING DATE: 2002-08-23
; PRIOR APPLICATION NUMBER: GB 0004576.5
; PRIOR FILING DATE: 2000-02-25
; PRIOR APPLICATION NUMBER: GB 0031341.1
; PRIOR FILING DATE: 2000-12-21
; NUMBER OF SEQ ID NOS: 110
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 68
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-227-616-68
```

```
Query Match          27.3%; Score 3; DB 14; Length 11;
Best Local Similarity 100.0%; Pred. No. 6.4e+03;
Matches      3; Conservative      0; Mismatches      0; Indels      0; Gaps      0;
```

Qy 9 AIK 11  
|||  
Db 9 AIK 11

RESULT 44

US-10-211-088-202  
; Sequence 202, Application US/10211088  
; Publication No. US20030104479A1  
; GENERAL INFORMATION:  
; APPLICANT: Bright, Gary R.  
; APPLICANT: Premkumar, D. David  
; APPLICANT: Chen, Yih-Tai  
; TITLE OF INVENTION: No. US20030104479A1 Fusion Proteins And Assays For  
Molecular Binding  
; FILE REFERENCE: 01-1022-US  
; CURRENT APPLICATION NUMBER: US/10/211,088  
; CURRENT FILING DATE: 2002-10-15  
; PRIOR APPLICATION NUMBER: 60/309,395  
; PRIOR FILING DATE: 2001-08-01  
; PRIOR APPLICATION NUMBER: 60/341,589  
; PRIOR FILING DATE: 2001-12-13  
; NUMBER OF SEQ ID NOS: 366  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 202  
; LENGTH: 11  
; TYPE: PRT  
; ORGANISM: Artificial sequence  
; FEATURE:  
; OTHER INFORMATION: Nuclear localization signal  
US-10-211-088-202

Query Match 27.3%; Score 3; DB 14; Length 11;  
Best Local Similarity 100.0%; Pred. No. 6.4e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 RKS 4  
|||  
Db 4 RKS 6

RESULT 45

US-10-136-738-2  
; Sequence 2, Application US/10136738  
; Publication No. US20030108886A1  
; GENERAL INFORMATION:  
; APPLICANT: Finn, John  
; APPLICANT: MacLachlan, Ian  
; APPLICANT: Protiva Biotherapeutics Inc.  
; TITLE OF INVENTION: Autogene Nucleic Acids Encoding a  
; TITLE OF INVENTION: Secretable RNA Polymerase  
; FILE REFERENCE: 020801-000310US  
; CURRENT APPLICATION NUMBER: US/10/136,738  
; CURRENT FILING DATE: 2002-04-30  
; PRIOR APPLICATION NUMBER: US 60/287,974  
; PRIOR FILING DATE: 2001-04-30  
; NUMBER OF SEQ ID NOS: 47

; SOFTWARE: FastSEQ for Windows Version 3.0  
; SEQ ID NO 2  
; LENGTH: 11  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: HIV-Tat variant secretion domain  
US-10-136-738-2

Query Match 27.3%; Score 3; DB 14; Length 11;  
Best Local Similarity 100.0%; Pred. No. 6.4e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ARK 3  
|||  
Db 2 ARK 4

RESULT 46

US-10-213-512-212  
; Sequence 212, Application US/10213512  
; Publication No. US20030110536A1  
; GENERAL INFORMATION:  
; APPLICANT: Fischer, Robert L.  
; APPLICANT: Ohad, Nir  
; APPLICANT: Kiyosue, Tomohiro  
; APPLICANT: Yadegari, Ramin  
; APPLICANT: Margossian, Linda  
; APPLICANT: Harada, John  
; APPLICANT: Goldberg, Robert B.  
; APPLICANT: The Regents of the University of California  
; TITLE OF INVENTION: Combinations of Nucleic Acids That Control Seed and  
; TITLE OF INVENTION: Fruit Development in Plants  
; FILE REFERENCE: 023070-086110US  
; CURRENT APPLICATION NUMBER: US/10/213,512  
; CURRENT FILING DATE: 2002-08-06  
; PRIOR APPLICATION NUMBER: US/09/177,206  
; PRIOR FILING DATE: 1998-10-22  
; PRIOR APPLICATION NUMBER: US 09/071,838  
; PRIOR FILING DATE: 1998-05-01  
; NUMBER OF SEQ ID NOS: 324  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 212  
; LENGTH: 11  
; TYPE: PRT  
; ORGANISM: Arabidopsis sp.  
US-10-213-512-212

Query Match 27.3%; Score 3; DB 14; Length 11;  
Best Local Similarity 100.0%; Pred. No. 6.4e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 RKS 4  
|||  
Db 2 RKS 4

RESULT 47

US-10-165-732A-10

; Sequence 10, Application US/10165732A  
 ; Publication No. US20030124117A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Refino, Canio J.  
 ; APPLICANT: Bunting, Stuart  
 ; APPLICANT: Kirchhofer, Daniel  
 ; TITLE OF INVENTION: COMBINATIONS OF ANTI-TISSUE FACTOR ANTIBODIES AND  
 ANTICOAGULANT AND/OR  
 ; TITLE OF INVENTION: ANTIPLATELET AGENTS  
 ; FILE REFERENCE: 11669.110USI1  
 ; CURRENT APPLICATION NUMBER: US/10/165,732A  
 ; CURRENT FILING DATE: 2002-11-13  
 ; PRIOR APPLICATION NUMBER: US 09/802,083  
 ; PRIOR FILING DATE: 2001-03-08  
 ; PRIOR APPLICATION NUMBER: US 60/189,775  
 ; PRIOR FILING DATE: 2000-03-16  
 ; NUMBER OF SEQ ID NOS: 28  
 ; SOFTWARE: PatentIn version 3.1  
 ; SEQ ID NO 10  
 ; LENGTH: 11  
 ; TYPE: PRT  
 ; ORGANISM: Mus musculus  
 US-10-165-732A-10

Query Match 27.3%; Score 3; DB 14; Length 11;  
 Best Local Similarity 100.0%; Pred. No. 6.4e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 SRD 6  
 |||  
 Db 3 SRD 5

RESULT 48

US-10-172-785-10

; Sequence 10, Application US/10172785  
 ; Publication No. US20030143225A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Refino, Canio J.  
 ; APPLICANT: Bunting, Stuart  
 ; APPLICANT: Kirchhofer, Daniel  
 ; TITLE OF INVENTION: COMBINATIONS OF ANTI-TISSUE FACTOR ANTIBODIES AND  
 ANTICOAGULANT AND/OR  
 ; TITLE OF INVENTION: ANTIPLATELET AGENTS  
 ; FILE REFERENCE: 11669.110USI2  
 ; CURRENT APPLICATION NUMBER: US/10/172,785  
 ; CURRENT FILING DATE: 2002-12-10  
 ; PRIOR APPLICATION NUMBER: US 10/165,732  
 ; PRIOR FILING DATE: 2002-06-07  
 ; PRIOR APPLICATION NUMBER: US 09/802,083  
 ; PRIOR FILING DATE: 2001-03-08  
 ; PRIOR APPLICATION NUMBER: US 60/189,775  
 ; PRIOR FILING DATE: 2000-03-16  
 ; NUMBER OF SEQ ID NOS: 28  
 ; SOFTWARE: PatentIn version 3.1



; SEQ ID NO 10  
; LENGTH: 11  
; TYPE: PRT  
; ORGANISM: Mus musculus  
US-10-172-785-10

Query Match 27.3%; Score 3; DB 14; Length 11;  
Best Local Similarity 100.0%; Pred. No. 6.4e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 SRD 6  
|||  
Db 3 SRD 5

RESULT 49

US-10-322-210-4

; Sequence 4, Application US/10322210  
; Publication No. US20030147906A1  
; GENERAL INFORMATION:  
; APPLICANT: Friede, Martin  
; APPLICANT: Mason, Sean  
; APPLICANT: Turnell, William Gordon  
; APPLICANT: Van Mechelen, Marcelle Paulette  
; APPLICANT: Vinals y de Bassols, Carlota  
; TITLE OF INVENTION: Epitopes or Mimotopes Derived from the  
; TITLE OF INVENTION: C-Epsilon-3 or C-Epsilon-4 Domains of IgE, Antagonists  
; TITLE OF INVENTION: Thereof, and Their Therapeutic Uses  
; FILE REFERENCE: B45173  
; CURRENT APPLICATION NUMBER: US/10/322,210  
; CURRENT FILING DATE: 2002-12-18  
; PRIOR APPLICATION NUMBER: US/09/914,089  
; PRIOR FILING DATE: 2001-08-22  
; PRIOR APPLICATION NUMBER: GB 9904408.3  
; PRIOR FILING DATE: 1999-02-25  
; PRIOR APPLICATION NUMBER: GB 9917144.9  
; PRIOR FILING DATE: 1999-07-21  
; PRIOR APPLICATION NUMBER: GB 9918598.5  
; PRIOR FILING DATE: 1999-08-07  
; PRIOR APPLICATION NUMBER: GB 9918599.3  
; PRIOR FILING DATE: 1999-08-07  
; PRIOR APPLICATION NUMBER: GB 9918601.7  
; PRIOR FILING DATE: 1999-08-07  
; PRIOR APPLICATION NUMBER: GB 9918604.1  
; PRIOR FILING DATE: 1999-08-07  
; PRIOR APPLICATION NUMBER: GB 9918606.6  
; PRIOR FILING DATE: 1999-08-07  
; PRIOR APPLICATION NUMBER: GB 9925618.2  
; PRIOR FILING DATE: 1999-10-29  
; NUMBER OF SEQ ID NOS: 86  
; SOFTWARE: FastSEQ for Windows Version 4.0  
; SEQ ID NO 4  
; LENGTH: 11  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Chimeric

US-10-322-210-4

Query Match 27.3%; Score 3; DB 14; Length 11;  
Best Local Similarity 100.0%; Pred. No. 6.4e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 SRD 6  
|||  
Db 6 SRD 8

RESULT 50

US-10-077-065-2

; Sequence 2, Application US/10077065  
; Publication No. US20030165501A1  
; GENERAL INFORMATION:  
; APPLICANT: DeAlmeida, Venita I., Stewart, Timothy A.  
; TITLE OF INVENTION: TREATMENT INVOLVING DKK-1 OR ANTAGONISTS THEREOF  
; FILE REFERENCE: P1872R1  
; CURRENT APPLICATION NUMBER: US/10/077,065  
; CURRENT FILING DATE: 2002-02-15  
; PRIOR APPLICATION NUMBER: US 60/269,435  
; PRIOR FILING DATE: 2001-02-16  
; NUMBER OF SEQ ID NOS: 3  
; SEQ ID NO 2  
; LENGTH: 11  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-077-065-2

Query Match 27.3%; Score 3; DB 14; Length 11;  
Best Local Similarity 100.0%; Pred. No. 6.4e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 AIK 11  
|||  
Db 7 AIK 9

RESULT 51

US-10-304-443-4

; Sequence 4, Application US/10304443  
; Publication No. US20030170229A1  
; GENERAL INFORMATION:  
; APPLICANT: Smithkline Beecham Biologicals s.a.  
; APPLICANT: Peptide Therapeutics Ltd.  
; TITLE OF INVENTION: Vaccine  
; FILE REFERENCE: B45173CIP  
; CURRENT APPLICATION NUMBER: US/10/304,443  
; CURRENT FILING DATE: 2002-11-26  
; PRIOR APPLICATION NUMBER: US/09/698,906A  
; PRIOR FILING DATE: 2001-02-20  
; NUMBER OF SEQ ID NOS: 121  
; SOFTWARE: FastSEQ for Windows Version 3.0  
; SEQ ID NO 4  
; LENGTH: 11  
; TYPE: PRT

; ORGANISM: Human peptide sequence  
US-10-304-443-4

Query Match 27.3%; Score 3; DB 14; Length 11;  
Best Local Similarity 100.0%; Pred. No. 6.4e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 SRD 6  
|||  
Db 6 SRD 8

RESULT 52

US-10-008-524A-171  
; Sequence 171, Application US/10008524A  
; Publication No. US20030175682A1  
; GENERAL INFORMATION:  
; APPLICANT: Doorbar, John  
; TITLE OF INVENTION: IMPROVEMENTS IN OR RELATING TO SCREENING FOR PAPILLOMA  
; TITLE OF INVENTION: VIRUSES  
; FILE REFERENCE: 18396/1074  
; CURRENT APPLICATION NUMBER: US/10/008,524A  
; CURRENT FILING DATE: 2002-08-13  
; PRIOR APPLICATION NUMBER: 09/314,268  
; PRIOR FILING DATE: 1999-05-18  
; NUMBER OF SEQ ID NOS: 179  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 171  
; LENGTH: 11  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
; OTHER INFORMATION: Peptide  
US-10-008-524A-171

Query Match 27.3%; Score 3; DB 14; Length 11;  
Best Local Similarity 100.0%; Pred. No. 6.4e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 SRD 6  
|||  
Db 2 SRD 4

RESULT 53

US-10-168-445-83  
; Sequence 83, Application US/10168445  
; Publication No. US20030177518A1  
; GENERAL INFORMATION:  
; APPLICANT: Osbourn, Anne E  
; APPLICANT: Haralampidis, Kosmas  
; APPLICANT: Bryan, Gregory T  
; TITLE OF INVENTION: Plant Gene  
; FILE REFERENCE: 0380-P02892US0  
; CURRENT APPLICATION NUMBER: US/10/168,445  
; CURRENT FILING DATE: 2002-10-30

; PRIOR APPLICATION NUMBER: PCT/GB00/04908  
; PRIOR FILING DATE: 2000-12-20  
; PRIOR APPLICATION NUMBER: GB 9930394.3  
; PRIOR FILING DATE: 1999-12-22  
; PRIOR APPLICATION NUMBER: GB 0020217.6  
; PRIOR FILING DATE: 2000-08-16  
; NUMBER OF SEQ ID NOS: 219  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 83  
; LENGTH: 11  
; TYPE: PRT  
; ORGANISM: Avena strigosa  
US-10-168-445-83

Query Match 27.3%; Score 3; DB 14; Length 11;  
Best Local Similarity 100.0%; Pred. No. 6.4e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 RKS 4  
|||  
Db 7 RKS 9

RESULT 54

US-10-405-339-13

; Sequence 13, Application US/10405339  
; Publication No. US20030190364A1  
; GENERAL INFORMATION:  
; APPLICANT: Panitch, Alyssa  
; APPLICANT: Seal, Brandon  
; TITLE OF INVENTION: Biological Affinity Based Delivery Systems  
; FILE REFERENCE: 9138-0079US  
; CURRENT APPLICATION NUMBER: US/10/405,339  
; CURRENT FILING DATE: 2003-04-01  
; PRIOR APPLICATION NUMBER: US 60/369,568  
; PRIOR FILING DATE: 2002-04-01  
; NUMBER OF SEQ ID NOS: 60  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 13  
; LENGTH: 11  
; TYPE: PRT  
; ORGANISM: Artificial sequence  
; FEATURE:  
; OTHER INFORMATION: Synthetic peptide  
US-10-405-339-13

Query Match 27.3%; Score 3; DB 14; Length 11;  
Best Local Similarity 100.0%; Pred. No. 6.4e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ARK 3  
|||  
Db 2 ARK 4

RESULT 55

US-10-376-121A-56

```

; Sequence 56, Application US/10376121A
; Publication No. US20030216544A1
; GENERAL INFORMATION:
;   APPLICANT: Harley, John
;   TITLE OF INVENTION: METHODS AND REAGENTS FOR DIAGNOSIS OF
;                       AUTOANTIBODIES
;   NUMBER OF SEQUENCES: 218
;   CORRESPONDENCE ADDRESS:
;       ADDRESSEE: Patrea L. Pabst
;       STREET: Suite 2000, 1201 West Peachtree Street, N.E.
;       CITY: Atlanta
;       STATE: GA
;       COUNTRY: USA
;       ZIP: 30309-3400
;   COMPUTER READABLE FORM:
;       MEDIUM TYPE: Floppy disk
;       COMPUTER: IBM PC compatible
;       OPERATING SYSTEM: PC-DOS/MS-DOS
;       SOFTWARE: PatentIn Release #1.0, Version #1.25
;   CURRENT APPLICATION DATA:
;       APPLICATION NUMBER: US/10/376,121A
;       FILING DATE: 27-Mar-2003
;       CLASSIFICATION: <Unknown>
;   PRIOR APPLICATION DATA:
;       APPLICATION NUMBER: 07/867,819
;       FILING DATE: April 13, 1992
;       APPLICATION NUMBER: 07/648,205
;       FILING DATE: January 31, 1991
;       APPLICATION NUMBER: 07/472,947
;       FILING DATE: January 31, 1990
;   ATTORNEY/AGENT INFORMATION:
;       NAME: Pabst, Patrea L.
;       REGISTRATION NUMBER: 31,284
;       REFERENCE/DOCKET NUMBER: OMRF114CIP(2)DIV(2)
;   TELECOMMUNICATION INFORMATION:
;       TELEPHONE: (404)-817-8473
;       TELEFAX: (404)-817-8588
;   INFORMATION FOR SEQ ID NO: 56:
;       SEQUENCE CHARACTERISTICS:
;           LENGTH: 11 amino acids
;           TYPE: amino acid
;           STRANDEDNESS: single
;           TOPOLOGY: linear
;       MOLECULE TYPE: peptide
;       FEATURE:
;           NAME/KEY: Binding-site
;           LOCATION: 1..8
;       SEQUENCE DESCRIPTION: SEQ ID NO: 56:
US-10-376-121A-56

```

```

Query Match          27.3%; Score 3; DB 15; Length 11;
Best Local Similarity 100.0%; Pred. No. 6.4e+03;
Matches      3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy      7 MTA 9
      |||
Db      9 MTA 11

```

RESULT 56

US-10-350-719-171

; Sequence 171, Application US/10350719  
 ; Publication No. US20030219726A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Doorbar, John  
 ; TITLE OF INVENTION: IMPROVEMENTS IN OR RELATING TO SCREENING FOR PAPILLOMA  
 ; TITLE OF INVENTION: VIRUSES  
 ; FILE REFERENCE: 18396/2162  
 ; CURRENT APPLICATION NUMBER: US/10/350,719  
 ; CURRENT FILING DATE: 2003-01-24  
 ; PRIOR APPLICATION NUMBER: PCT/GB01/01176  
 ; PRIOR FILING DATE: 2001-03-16  
 ; PRIOR APPLICATION NUMBER: GB0018140.4  
 ; PRIOR FILING DATE: 2000-07-24  
 ; NUMBER OF SEQ ID NOS: 180  
 ; SOFTWARE: PatentIn Ver. 2.1  
 ; SEQ ID NO 171  
 ; LENGTH: 11  
 ; TYPE: PRT  
 ; ORGANISM: Artificial Sequence  
 ; FEATURE:  
 ; OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
 ; OTHER INFORMATION: Peptide  
 US-10-350-719-171

Query Match 27.3%; Score 3; DB 15; Length 11;  
 Best Local Similarity 100.0%; Pred. No. 6.4e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 SRD 6  
 |||  
 Db 2 SRD 4

RESULT 57

US-10-378-173-136

; Sequence 136, Application US/10378173  
 ; Publication No. US20030232014A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Burke et al.  
 ; TITLE OF INVENTION: PHOSPHORYLATED PROTEINS AND USES RELATED THERETO  
 ; FILE REFERENCE: MDSP-P01-023  
 ; CURRENT APPLICATION NUMBER: US/10/378,173  
 ; CURRENT FILING DATE: 2003-03-03  
 ; PRIOR APPLICATION NUMBER: 60/360787  
 ; PRIOR FILING DATE: 2002-03-01  
 ; NUMBER OF SEQ ID NOS: 231  
 ; SOFTWARE: PatentIn version 3.2  
 ; SEQ ID NO 136  
 ; LENGTH: 11  
 ; TYPE: PRT  
 ; ORGANISM: Artificial Sequence  
 ; FEATURE:  
 ; OTHER INFORMATION: phosphorylated peptide

; FEATURE:  
; NAME/KEY: MISC\_FEATURE  
; LOCATION: (3)..(3)  
; OTHER INFORMATION: phosphorylation  
; FEATURE:  
; NAME/KEY: MISC\_FEATURE  
; LOCATION: (4)..(4)  
; OTHER INFORMATION: phosphorylation  
US-10-378-173-136

Query Match 27.3%; Score 3; DB 15; Length 11;  
Best Local Similarity 100.0%; Pred. No. 6.4e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 RKS 4  
|||  
Db 1 RKS 3

RESULT 58

US-10-032-037B-5

; Sequence 5, Application US/10032037B  
; Publication No. US20040001822A1  
; GENERAL INFORMATION:  
; APPLICANT: Bio-Technology General Corp.  
; TITLE OF INVENTION: Y17-ISOLATED MOLECULES COMPRISING EPITOPES CONTAINING SULFATED  
; TITLE OF INVENTION: MOIETIES, ANTIBODIES TO SUCH EPITOPES, AND USES THEREOF  
; FILE REFERENCE: 10793/44  
; CURRENT APPLICATION NUMBER: US/10/032,037B  
; CURRENT FILING DATE: 2001-12-31  
; PRIOR APPLICATION NUMBER: 60/258,948  
; PRIOR FILING DATE: 2000-12-29  
; NUMBER OF SEQ ID NOS: 204  
; SOFTWARE: FastSEQ for Windows Version 3.0  
; SEQ ID NO 5  
; LENGTH: 11  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-032-037B-5

Query Match 27.3%; Score 3; DB 15; Length 11;  
Best Local Similarity 100.0%; Pred. No. 6.4e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 SRD 6  
|||  
Db 2 SRD 4

RESULT 59

US-10-032-037B-118

; Sequence 118, Application US/10032037B  
; Publication No. US20040001822A1  
; GENERAL INFORMATION:  
; APPLICANT: Bio-Technology General Corp.

```
; TITLE OF INVENTION: Y17-ISOLATED MOLECULES COMPRISING EPITOPES CONTAINING
SULFATED
; TITLE OF INVENTION: MOIETIES, ANTIBODIES TO SUCH EPITOPES, AND USES THEREOF
; FILE REFERENCE: 10793/44
; CURRENT APPLICATION NUMBER: US/10/032,037B
; CURRENT FILING DATE: 2001-12-31
; PRIOR APPLICATION NUMBER: 60/258,948
; PRIOR FILING DATE: 2000-12-29
; NUMBER OF SEQ ID NOS: 204
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 118
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-032-037B-118
```

```
Query Match          27.3%; Score 3; DB 15; Length 11;
Best Local Similarity 100.0%; Pred. No. 6.4e+03;
Matches      3; Conservative    0; Mismatches    0; Indels      0; Gaps      0;
```

```
Qy          4 SRD 6
            |||
Db          5 SRD 7
```

# RESULT 60

```
US-10-032-037B-131
; Sequence 131, Application US/10032037B
; Publication No. US20040001822A1
; GENERAL INFORMATION:
; APPLICANT: Bio-Technology General Corp.
; TITLE OF INVENTION: Y17-ISOLATED MOLECULES COMPRISING EPITOPES CONTAINING
SULFATED
; TITLE OF INVENTION: MOIETIES, ANTIBODIES TO SUCH EPITOPES, AND USES THEREOF
; FILE REFERENCE: 10793/44
; CURRENT APPLICATION NUMBER: US/10/032,037B
; CURRENT FILING DATE: 2001-12-31
; PRIOR APPLICATION NUMBER: 60/258,948
; PRIOR FILING DATE: 2000-12-29
; NUMBER OF SEQ ID NOS: 204
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 131
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-032-037B-131
```

```
Query Match          27.3%; Score 3; DB 15; Length 11;
Best Local Similarity 100.0%; Pred. No. 6.4e+03;
Matches      3; Conservative    0; Mismatches    0; Indels      0; Gaps      0;
```

```
Qy          4 SRD 6
            |||
Db          2 SRD 4
```

# RESULT 61



US-10-032-037B-133  
 ; Sequence 133, Application US/10032037B  
 ; Publication No. US20040001822A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Bio-Technology General Corp.  
 ; TITLE OF INVENTION: Y17-ISOLATED MOLECULES COMPRISING EPITOPES CONTAINING  
 SULFATED  
 ; TITLE OF INVENTION: MOIETIES, ANTIBODIES TO SUCH EPITOPES, AND USES THEREOF  
 ; FILE REFERENCE: 10793/44  
 ; CURRENT APPLICATION NUMBER: US/10/032,037B  
 ; CURRENT FILING DATE: 2001-12-31  
 ; PRIOR APPLICATION NUMBER: 60/258,948  
 ; PRIOR FILING DATE: 2000-12-29  
 ; NUMBER OF SEQ ID NOS: 204  
 ; SOFTWARE: FastSEQ for Windows Version 3.0  
 ; SEQ ID NO 133  
 ; LENGTH: 11  
 ; TYPE: PRT  
 ; ORGANISM: Homo sapiens  
 US-10-032-037B-133

Query Match 27.3%; Score 3; DB 15; Length 11;  
 Best Local Similarity 100.0%; Pred. No. 6.4e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 SRD 6  
 |||  
 Db 2 SRD 4

RESULT 62  
 US-10-032-037B-139  
 ; Sequence 139, Application US/10032037B  
 ; Publication No. US20040001822A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Bio-Technology General Corp.  
 ; TITLE OF INVENTION: Y17-ISOLATED MOLECULES COMPRISING EPITOPES CONTAINING  
 SULFATED  
 ; TITLE OF INVENTION: MOIETIES, ANTIBODIES TO SUCH EPITOPES, AND USES THEREOF  
 ; FILE REFERENCE: 10793/44  
 ; CURRENT APPLICATION NUMBER: US/10/032,037B  
 ; CURRENT FILING DATE: 2001-12-31  
 ; PRIOR APPLICATION NUMBER: 60/258,948  
 ; PRIOR FILING DATE: 2000-12-29  
 ; NUMBER OF SEQ ID NOS: 204  
 ; SOFTWARE: FastSEQ for Windows Version 3.0  
 ; SEQ ID NO 139  
 ; LENGTH: 11  
 ; TYPE: PRT  
 ; ORGANISM: Homo sapiens  
 US-10-032-037B-139

Query Match 27.3%; Score 3; DB 15; Length 11;  
 Best Local Similarity 100.0%; Pred. No. 6.4e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 SRD 6

Db            |||  
             2 SRD 4

RESULT 63

US-10-032-037B-161  
; Sequence 161, Application US/10032037B  
; Publication No. US20040001822A1  
; GENERAL INFORMATION:  
; APPLICANT: Bio-Technology General Corp.  
; TITLE OF INVENTION: Y17-ISOLATED MOLECULES COMPRISING EPITOPES CONTAINING  
SULFATED  
; TITLE OF INVENTION: MOIETIES, ANTIBODIES TO SUCH EPITOPES, AND USES THEREOF  
; FILE REFERENCE: 10793/44  
; CURRENT APPLICATION NUMBER: US/10/032,037B  
; CURRENT FILING DATE: 2001-12-31  
; PRIOR APPLICATION NUMBER: 60/258,948  
; PRIOR FILING DATE: 2000-12-29  
; NUMBER OF SEQ ID NOS: 204  
; SOFTWARE: FastSEQ for Windows Version 3.0  
; SEQ ID NO 161  
; LENGTH: 11  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-032-037B-161

Query Match                    27.3%; Score 3; DB 15; Length 11;  
Best Local Similarity       100.0%; Pred. No. 6.4e+03;  
Matches       3; Conservative       0; Mismatches       0; Indels       0; Gaps       0;

Qy            4 SRD 6  
             |||  
Db            2 SRD 4

RESULT 64

US-10-032-037B-202  
; Sequence 202, Application US/10032037B  
; Publication No. US20040001822A1  
; GENERAL INFORMATION:  
; APPLICANT: Bio-Technology General Corp.  
; TITLE OF INVENTION: Y17-ISOLATED MOLECULES COMPRISING EPITOPES CONTAINING  
SULFATED  
; TITLE OF INVENTION: MOIETIES, ANTIBODIES TO SUCH EPITOPES, AND USES THEREOF  
; FILE REFERENCE: 10793/44  
; CURRENT APPLICATION NUMBER: US/10/032,037B  
; CURRENT FILING DATE: 2001-12-31  
; PRIOR APPLICATION NUMBER: 60/258,948  
; PRIOR FILING DATE: 2000-12-29  
; NUMBER OF SEQ ID NOS: 204  
; SOFTWARE: FastSEQ for Windows Version 3.0  
; SEQ ID NO 202  
; LENGTH: 11  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-032-037B-202

Query Match 27.3%; Score 3; DB 15; Length 11;  
Best Local Similarity 100.0%; Pred. No. 6.4e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 SRD 6  
|||  
Db 2 SRD 4

RESULT 65

US-10-029-988B-5

; Sequence 5, Application US/10029988B  
; Publication No. US20040001839A1  
; GENERAL INFORMATION:  
; APPLICANT: Bio-Technology General Corp.  
; TITLE OF INVENTION: Y17-ISOLATED MOLECULES COMPRISING EPITOPES CONTAINING  
SULFATED  
; TITLE OF INVENTION: MOIETIES, ANTIBODIES TO SUCH EPITOPES, AND USES THEREOF  
; FILE REFERENCE: 10793/46  
; CURRENT APPLICATION NUMBER: US/10/029,988B  
; CURRENT FILING DATE: 2001-12-31  
; PRIOR APPLICATION NUMBER: 60/258,948  
; PRIOR FILING DATE: 2000-12-29  
; NUMBER OF SEQ ID NOS: 204  
; SOFTWARE: FastSEQ for Windows Version 3.0  
; SEQ ID NO 5  
; LENGTH: 11  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-029-988B-5

Query Match 27.3%; Score 3; DB 15; Length 11;  
Best Local Similarity 100.0%; Pred. No. 6.4e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 SRD 6  
|||  
Db 2 SRD 4

RESULT 66

US-10-029-988B-118

; Sequence 118, Application US/10029988B  
; Publication No. US20040001839A1  
; GENERAL INFORMATION:  
; APPLICANT: Bio-Technology General Corp.  
; TITLE OF INVENTION: Y17-ISOLATED MOLECULES COMPRISING EPITOPES CONTAINING  
SULFATED  
; TITLE OF INVENTION: MOIETIES, ANTIBODIES TO SUCH EPITOPES, AND USES THEREOF  
; FILE REFERENCE: 10793/46  
; CURRENT APPLICATION NUMBER: US/10/029,988B  
; CURRENT FILING DATE: 2001-12-31  
; PRIOR APPLICATION NUMBER: 60/258,948  
; PRIOR FILING DATE: 2000-12-29  
; NUMBER OF SEQ ID NOS: 204  
; SOFTWARE: FastSEQ for Windows Version 3.0  
; SEQ ID NO 118

; LENGTH: 11  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-029-988B-118

Query Match 27.3%; Score 3; DB 15; Length 11;  
Best Local Similarity 100.0%; Pred. No. 6.4e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 SRD 6  
|||  
Db 5 SRD 7

RESULT 67

US-10-029-988B-131  
; Sequence 131, Application US/10029988B  
; Publication No. US20040001839A1  
; GENERAL INFORMATION:  
; APPLICANT: Bio-Technology General Corp.  
; TITLE OF INVENTION: Y17-ISOLATED MOLECULES COMPRISING EPITOPES CONTAINING  
SULFATED  
; TITLE OF INVENTION: MOIETIES, ANTIBODIES TO SUCH EPITOPES, AND USES THEREOF  
; FILE REFERENCE: 10793/46  
; CURRENT APPLICATION NUMBER: US/10/029,988B  
; CURRENT FILING DATE: 2001-12-31  
; PRIOR APPLICATION NUMBER: 60/258,948  
; PRIOR FILING DATE: 2000-12-29  
; NUMBER OF SEQ ID NOS: 204  
; SOFTWARE: FastSEQ for Windows Version 3.0  
; SEQ ID NO 131  
; LENGTH: 11  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-029-988B-131

Query Match 27.3%; Score 3; DB 15; Length 11;  
Best Local Similarity 100.0%; Pred. No. 6.4e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 SRD 6  
|||  
Db 2 SRD 4

RESULT 68

US-10-029-988B-133  
; Sequence 133, Application US/10029988B  
; Publication No. US20040001839A1  
; GENERAL INFORMATION:  
; APPLICANT: Bio-Technology General Corp.  
; TITLE OF INVENTION: Y17-ISOLATED MOLECULES COMPRISING EPITOPES CONTAINING  
SULFATED  
; TITLE OF INVENTION: MOIETIES, ANTIBODIES TO SUCH EPITOPES, AND USES THEREOF  
; FILE REFERENCE: 10793/46  
; CURRENT APPLICATION NUMBER: US/10/029,988B  
; CURRENT FILING DATE: 2001-12-31

; PRIOR APPLICATION NUMBER: 60/258,948  
; PRIOR FILING DATE: 2000-12-29  
; NUMBER OF SEQ ID NOS: 204  
; SOFTWARE: FastSEQ for Windows Version 3.0  
; SEQ ID NO 133  
; LENGTH: 11  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-029-988B-133

Query Match 27.3%; Score 3; DB 15; Length 11;  
Best Local Similarity 100.0%; Pred. No. 6.4e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 SRD 6  
| | |  
Db 2 SRD 4

RESULT 69

US-10-029-988B-139  
; Sequence 139, Application US/10029988B  
; Publication No. US20040001839A1  
; GENERAL INFORMATION:  
; APPLICANT: Bio-Technology General Corp.  
; TITLE OF INVENTION: Y17-ISOLATED MOLECULES COMPRISING EPITOPES CONTAINING  
SULFATED  
; TITLE OF INVENTION: MOIETIES, ANTIBODIES TO SUCH EPITOPES, AND USES THEREOF  
; FILE REFERENCE: 10793/46  
; CURRENT APPLICATION NUMBER: US/10/029,988B  
; CURRENT FILING DATE: 2001-12-31  
; PRIOR APPLICATION NUMBER: 60/258,948  
; PRIOR FILING DATE: 2000-12-29  
; NUMBER OF SEQ ID NOS: 204  
; SOFTWARE: FastSEQ for Windows Version 3.0  
; SEQ ID NO 139  
; LENGTH: 11  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-029-988B-139

Query Match 27.3%; Score 3; DB 15; Length 11;  
Best Local Similarity 100.0%; Pred. No. 6.4e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 SRD 6  
| | |  
Db 2 SRD 4

RESULT 70

US-10-029-988B-161  
; Sequence 161, Application US/10029988B  
; Publication No. US20040001839A1  
; GENERAL INFORMATION:  
; APPLICANT: Bio-Technology General Corp.

```
; TITLE OF INVENTION: Y17-ISOLATED MOLECULES COMPRISING EPITOPES CONTAINING
SULFATED
; TITLE OF INVENTION: MOIETIES, ANTIBODIES TO SUCH EPITOPES, AND USES THEREOF
; FILE REFERENCE: 10793/46
; CURRENT APPLICATION NUMBER: US/10/029,988B
; CURRENT FILING DATE: 2001-12-31
; PRIOR APPLICATION NUMBER: 60/258,948
; PRIOR FILING DATE: 2000-12-29
; NUMBER OF SEQ ID NOS: 204
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 161
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-029-988B-161
```

```
Query Match          27.3%; Score 3; DB 15; Length 11;
Best Local Similarity 100.0%; Pred. No. 6.4e+03;
Matches      3; Conservative      0; Mismatches      0; Indels      0; Gaps      0;
```

```
Qy      4 SRD 6
      |||
Db      2 SRD 4
```

#### RESULT 71

```
US-10-029-988B-202
; Sequence 202, Application US/10029988B
; Publication No. US20040001839A1
; GENERAL INFORMATION:
; APPLICANT: Bio-Technology General Corp.
; TITLE OF INVENTION: Y17-ISOLATED MOLECULES COMPRISING EPITOPES CONTAINING
SULFATED
; TITLE OF INVENTION: MOIETIES, ANTIBODIES TO SUCH EPITOPES, AND USES THEREOF
; FILE REFERENCE: 10793/46
; CURRENT APPLICATION NUMBER: US/10/029,988B
; CURRENT FILING DATE: 2001-12-31
; PRIOR APPLICATION NUMBER: 60/258,948
; PRIOR FILING DATE: 2000-12-29
; NUMBER OF SEQ ID NOS: 204
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 202
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-029-988B-202
```

```
Query Match          27.3%; Score 3; DB 15; Length 11;
Best Local Similarity 100.0%; Pred. No. 6.4e+03;
Matches      3; Conservative      0; Mismatches      0; Indels      0; Gaps      0;
```

```
Qy      4 SRD 6
      |||
Db      2 SRD 4
```

#### RESULT 72

US-10-032-423A-5

; Sequence 5, Application US/10032423A  
; Publication No. US20040002450A1  
; GENERAL INFORMATION:  
; APPLICANT: Bio-Technology General Corp.  
; TITLE OF INVENTION: Y17-ISOLATED MOLECULES COMPRISING EPITOPES CONTAINING  
SULFATED  
; TITLE OF INVENTION: MOIETIES, ANTIBODIES TO SUCH EPITOPES, AND USES THEREOF  
; FILE REFERENCE: 10793/45  
; CURRENT APPLICATION NUMBER: US/10/032,423A  
; CURRENT FILING DATE: 2001-12-31  
; PRIOR APPLICATION NUMBER: 60/258,948  
; PRIOR FILING DATE: 12/29/2000  
; NUMBER OF SEQ ID NOS: 204  
; SOFTWARE: FastSEQ for Windows Version 3.0  
; SEQ ID NO 5  
; LENGTH: 11  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-032-423A-5

Query Match 27.3%; Score 3; DB 15; Length 11;  
Best Local Similarity 100.0%; Pred. No. 6.4e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 SRD 6  
|||  
Db 2 SRD 4

RESULT 73

US-10-032-423A-118

; Sequence 118, Application US/10032423A  
; Publication No. US20040002450A1  
; GENERAL INFORMATION:  
; APPLICANT: Bio-Technology General Corp.  
; TITLE OF INVENTION: Y17-ISOLATED MOLECULES COMPRISING EPITOPES CONTAINING  
SULFATED  
; TITLE OF INVENTION: MOIETIES, ANTIBODIES TO SUCH EPITOPES, AND USES THEREOF  
; FILE REFERENCE: 10793/45  
; CURRENT APPLICATION NUMBER: US/10/032,423A  
; CURRENT FILING DATE: 2001-12-31  
; PRIOR APPLICATION NUMBER: 60/258,948  
; PRIOR FILING DATE: 12/29/2000  
; NUMBER OF SEQ ID NOS: 204  
; SOFTWARE: FastSEQ for Windows Version 3.0  
; SEQ ID NO 118  
; LENGTH: 11  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-032-423A-118

Query Match 27.3%; Score 3; DB 15; Length 11;  
Best Local Similarity 100.0%; Pred. No. 6.4e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 SRD 6

Db                    |||  
                      5 SRD 7

RESULT 74

US-10-032-423A-131  
; Sequence 131, Application US/10032423A  
; Publication No. US20040002450A1  
; GENERAL INFORMATION:  
; APPLICANT: Bio-Technology General Corp.  
; TITLE OF INVENTION: Y17-ISOLATED MOLECULES COMPRISING EPITOPES CONTAINING  
SULFATED  
; TITLE OF INVENTION: MOIETIES, ANTIBODIES TO SUCH EPITOPES, AND USES THEREOF  
; FILE REFERENCE: 10793/45  
; CURRENT APPLICATION NUMBER: US/10/032,423A  
; CURRENT FILING DATE: 2001-12-31  
; PRIOR APPLICATION NUMBER: 60/258,948  
; PRIOR FILING DATE: 12/29/2000  
; NUMBER OF SEQ ID NOS: 204  
; SOFTWARE: FastSEQ for Windows Version 3.0  
; SEQ ID NO 131  
; LENGTH: 11  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-032-423A-131

Query Match                    27.3%; Score 3; DB 15; Length 11;  
Best Local Similarity        100.0%; Pred. No. 6.4e+03;  
Matches        3; Conservative        0; Mismatches        0; Indels        0; Gaps        0;

Qy                    4 SRD 6  
                      |||  
Db                    2 SRD 4

RESULT 75

US-10-032-423A-133  
; Sequence 133, Application US/10032423A  
; Publication No. US20040002450A1  
; GENERAL INFORMATION:  
; APPLICANT: Bio-Technology General Corp.  
; TITLE OF INVENTION: Y17-ISOLATED MOLECULES COMPRISING EPITOPES CONTAINING  
SULFATED  
; TITLE OF INVENTION: MOIETIES, ANTIBODIES TO SUCH EPITOPES, AND USES THEREOF  
; FILE REFERENCE: 10793/45  
; CURRENT APPLICATION NUMBER: US/10/032,423A  
; CURRENT FILING DATE: 2001-12-31  
; PRIOR APPLICATION NUMBER: 60/258,948  
; PRIOR FILING DATE: 12/29/2000  
; NUMBER OF SEQ ID NOS: 204  
; SOFTWARE: FastSEQ for Windows Version 3.0  
; SEQ ID NO 133  
; LENGTH: 11  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-032-423A-133



Query Match 27.3%; Score 3; DB 15; Length 11;  
Best Local Similarity 100.0%; Pred. No. 6.4e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 SRD 6  
|||  
Db 2 SRD 4

Search completed: April 8, 2004, 16:35:50  
Job time : 30.3077 secs

OM protein - protein search, using sw model

Run on: April 8, 2004, 15:30:07 ; Search time 27.7692 Seconds  
(without alignments)  
124.984 Million cell updates/sec

Title: US-09-787-443A-22  
Perfect score: 11  
Sequence: 1 ARKSRDMTAAIK 11

Scoring table: OLIGO  
Gapop 60.0 , Gapext 60.0

Searched: 1017041 seqs, 315518202 residues

Word size : 0

Total number of hits satisfying chosen parameters: 460

Minimum DB seq length: 11  
Maximum DB seq length: 11

Post-processing: Listing first 100 summaries

Database : SPTREMBL\_25:\*  
1: sp\_archaea:\*  
2: sp\_bacteria:\*  
3: sp\_fungi:\*  
4: sp\_human:\*  
5: sp\_invertebrate:\*  
6: sp\_mammal:\*  
7: sp\_mhc:\*  
8: sp\_organelle:\*  
9: sp\_phage:\*  
10: sp\_plant:\*  
11: sp\_rodent:\*  
12: sp\_virus:\*  
13: sp\_vertebrate:\*  
14: sp\_unclassified:\*  
15: sp\_rvirus:\*  
16: sp\_bacteriap:\*  
17: sp\_archeap:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

8

Result	Query					
No.	Score	Match	Length	DB	ID	Description
-----						

1	3	27.3	11	2	Q47602	Q47602	escherichia
2	2	18.2	11	2	Q9R790	Q9r790	borrelia ga
3	2	18.2	11	2	Q47451	Q47451	escherichia
4	2	18.2	11	2	Q9AIZ7	Q9aiz7	carsonella
5	2	18.2	11	2	Q8RKN1	Q8rkn1	escherichia
6	2	18.2	11	2	Q8L2T4	Q8l2t4	neisseria m
7	2	18.2	11	2	P77404	P77404	escherichia
8	2	18.2	11	2	Q8RMI8	Q8rmi8	enterococcu
9	2	18.2	11	2	Q44090	Q44090	acholeplasm
10	2	18.2	11	2	Q44237	Q44237	anabaena sp
11	2	18.2	11	2	Q9R872	Q9r872	escherichia
12	2	18.2	11	2	Q8GL24	Q8gl24	borrelia bu
13	2	18.2	11	2	Q8GL19	Q8gl19	borrelia bu
14	2	18.2	11	2	Q7WUL8	Q7wul8	pseudomonas
15	2	18.2	11	3	Q9URG1	Q9urg1	neurospora
16	2	18.2	11	3	Q96V15	Q96v15	cryptococcu
17	2	18.2	11	4	Q14759	Q14759	homo sapien
18	2	18.2	11	4	Q9NY38	Q9ny38	homo sapien
19	2	18.2	11	4	Q9Y3G2	Q9y3g2	homo sapien
20	2	18.2	11	4	Q9UNL8	Q9unl8	homo sapien
21	2	18.2	11	4	Q9UCP5	Q9ucp5	homo sapien
22	2	18.2	11	4	Q16234	Q16234	homo sapien
23	2	18.2	11	4	Q9UBM2	Q9ubm2	homo sapien
24	2	18.2	11	4	Q8NI03	Q8ni03	homo sapien
25	2	18.2	11	4	Q9UCR1	Q9ucr1	homo sapien
26	2	18.2	11	4	Q9HCN5	Q9hcn5	homo sapien
27	2	18.2	11	5	Q25916	Q25916	plasmodium
28	2	18.2	11	5	Q9NFX0	Q9nfx0	drosophila
29	2	18.2	11	5	Q8MPQ3	Q8mpq3	caenorhabdi
30	2	18.2	11	6	Q9TRR7	Q9trr7	oryctolagus
31	2	18.2	11	6	Q9XSP7	Q9xsp7	pygathrix n
32	2	18.2	11	6	Q9XSP2	Q9xsp2	hylobates s
33	2	18.2	11	6	Q9XSP5	Q9xsp5	pan troglod
34	2	18.2	11	6	Q9TQS9	Q9tqs9	equus cabal
35	2	18.2	11	6	Q9TQS0	Q9tqs0	bos taurus
36	2	18.2	11	6	Q9XSP8	Q9xsp8	presbytis j
37	2	18.2	11	6	Q9XSP6	Q9xsp6	pongo pygma
38	2	18.2	11	6	Q9XSQ4	Q9xsq4	gorilla gor
39	2	18.2	11	7	O77900	O77900	oreochromis
40	2	18.2	11	7	O77917	O77917	oreochromis
41	2	18.2	11	7	O77902	O77902	oreochromis
42	2	18.2	11	7	O77921	O77921	pseudotroph
43	2	18.2	11	7	O77901	O77901	oreochromis
44	2	18.2	11	7	O77916	O77916	oreochromis
45	2	18.2	11	7	O77905	O77905	oreochromis
46	2	18.2	11	7	O77899	O77899	oreochromis
47	2	18.2	11	7	O78121	O78121	oreochromis
48	2	18.2	11	7	O77904	O77904	oreochromis
49	2	18.2	11	7	O77903	O77903	oreochromis
50	2	18.2	11	8	Q94V94	Q94v94	varanus sto
51	2	18.2	11	8	Q8ME62	Q8me62	porphyra ca
52	2	18.2	11	8	Q9G5W2	Q9g5w2	laudakia tu
53	2	18.2	11	8	Q9G622	Q9g622	salea horsf
54	2	18.2	11	8	Q94VG8	Q94vg8	varanus gou
55	2	18.2	11	8	Q9G5Y6	Q9g5y6	agama agama
56	2	18.2	11	8	Q8MEL7	Q8mel7	sida hooker
57	2	18.2	11	8	Q9G5Y0	Q9g5y0	pseudotrape

58	2	18.2	11	8	Q9G5W5	Q9g5w5	laudakia	nu
59	2	18.2	11	8	Q9G607	Q9g607	aphaniotis	
60	2	18.2	11	8	Q94V77	Q94v77	heloderma	s
61	2	18.2	11	8	O79985	O79985	laudakia	ca
62	2	18.2	11	8	Q9G359	Q9g359	japalura	fl
63	2	18.2	11	8	Q8MEM2	Q8mem2	lagunaria	p
64	2	18.2	11	8	Q9G649	Q9g649	otocryptis	
65	2	18.2	11	8	Q9G643	Q9g643	calotes	cal
66	2	18.2	11	8	Q9G5X4	Q9g5x4	trapelus	ag
67	2	18.2	11	8	Q94V74	Q94v74	lanthanotus	
68	2	18.2	11	8	Q8MES5	Q8mes5	abelmoschus	
69	2	18.2	11	8	Q9GD68	Q9gd68	elaeis	guin
70	2	18.2	11	8	Q9G350	Q9g350	laudakia	sa
71	2	18.2	11	8	Q8WD17	Q8wd17	ctenophorus	
72	2	18.2	11	8	Q9G5Z8	Q9g5z8	acanthosaur	
73	2	18.2	11	8	Q9G368	Q9g368	draco	blanf
74	2	18.2	11	8	Q9G5W8	Q9g5w8	trapelus	sa
75	2	18.2	11	8	Q8MEP0	Q8mep0	hibiscus	pe
76	2	18.2	11	8	Q94VE7	Q94ve7	varanus	kom
77	2	18.2	11	8	Q94VB8	Q94vb8	varanus	sal
78	2	18.2	11	8	Q9G353	Q9g353	trapelus	sa
79	2	18.2	11	8	Q32704	Q32704	nicotiana	t
80	2	18.2	11	8	O79642	O79642	laudakia	mi
81	2	18.2	11	8	Q8MES1	Q8mes1	alyogyne	pi
82	2	18.2	11	8	Q94VH7	Q94vh7	varanus	gil
83	2	18.2	11	8	Q8SKR0	Q8skr0	rankinia	di
84	2	18.2	11	8	Q8MEP3	Q8mep3	hibiscus	no
85	2	18.2	11	8	Q9G619	Q9g619	ceratophora	
86	2	18.2	11	8	Q8WER7	Q8wer7	ceratophora	
87	2	18.2	11	8	Q8WD50	Q8wd50	ceratophora	
88	2	18.2	11	8	Q94VK1	Q94vk1	varanus	aca
89	2	18.2	11	8	Q9G356	Q9g356	agama	atra
90	2	18.2	11	8	O79639	O79639	laudakia	le
91	2	18.2	11	8	Q8MEQ7	Q8meq7	hibiscus	dr
92	2	18.2	11	8	Q9G5V0	Q9g5v0	laudakia	st
93	2	18.2	11	8	Q8MEL9	Q8mel9	pavonia	has
94	2	18.2	11	8	Q9G5X1	Q9g5x1	trapelus	pe
95	2	18.2	11	8	Q8MER0	Q8mer0	hibiscus	co
96	2	18.2	11	8	Q8MES3	Q8mes3	alyogyne	cr
97	2	18.2	11	8	Q9G658	Q9g658	hydrosaurus	
98	2	18.2	11	8	Q8ME54	Q8me54	porphyra	um
99	2	18.2	11	8	Q8WER4	Q8wer4	ceratophora	
100	2	18.2	11	8	Q8MEP5	Q8mep5	hibiscus	mi

#### ALIGNMENTS

#### RESULT 1

Q47602

ID Q47602 PRELIMINARY; PRT; 11 AA.

AC Q47602;

DT 01-NOV-1996 (TrEMBLrel. 01, Created)

DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)

DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)

DE REase protein (Fragment).

GN REASE.

OS Escherichia coli.  
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;  
 OC Enterobacteriaceae; Escherichia.  
 OX NCBI\_TaxID=562;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=91139577; PubMed=1995588;  
 RA Tao T., Bourne J.C., Blumenthal R.M.;  
 RT "A family of regulatory genes associated with type II restriction-  
 RT modification systems.";  
 RL J. Bacteriol. 173:1367-1375(1991).  
 DR EMBL; M63620; AAA24558.1; -.  
 FT NON\_TER 11 11  
 SQ SEQUENCE 11 AA; 1412 MW; 80ABB190C736DAAA CRC64;

Query Match 27.3%; Score 3; DB 2; Length 11;  
 Best Local Similarity 100.0%; Pred. No. 9.7e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 SRD 6  
 |||  
 Db 2 SRD 4

## RESULT 2

Q9R790

ID Q9R790 PRELIMINARY; PRT; 11 AA.  
 AC Q9R790;  
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)  
 DE Outer surface protein C (Fragment).  
 GN OSPC.  
 OS Borrelia garinii.  
 OC Bacteria; Spirochaetes; Spirochaetales; Spirochaetaceae; Borrelia.  
 OX NCBI\_TaxID=29519;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=G25;  
 RX MEDLINE=97426044; PubMed=9282748;  
 RA Tilly K., Casjens S., Stevenson B., Bono J.L., Samuels D.S., Hogan D.,  
 RA Rosa P.;  
 RT "he Borrelia burgdorferi circular plasmid cp26: conservation of  
 RT plasmid structure and targeted inactivation of the ospC gene.";  
 RL Mol. Microbiol. 25:361-374(1997).  
 DR EMBL; U93700; AAC45535.1; -.  
 DR GO; GO:0009279; C:external outer membrane (sensu Gram-negativ. . .; IEA.  
 DR GO; GO:0003793; F:defense/immunity protein activity; IEA.  
 DR GO; GO:0006952; P:defense response; IEA.  
 DR InterPro; IPR001800; Lipoprotein\_6.  
 DR Pfam; PF01441; Lipoprotein\_6; 1.  
 FT NON\_TER 11 11  
 SQ SEQUENCE 11 AA; 1250 MW; 0868D864C5B731A4 CRC64;

Query Match 18.2%; Score 2; DB 2; Length 11;  
 Best Local Similarity 100.0%; Pred. No. 1.2e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 AI 10  
||  
Db 8 AI 9

RESULT 3

Q47451

ID Q47451 PRELIMINARY; PRT; 11 AA.  
AC Q47451;  
DT 01-NOV-1996 (TrEMBLrel. 01, Created)  
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)  
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)  
DE Plasmid pRJ1004 DNA (Fragment).  
OS Escherichia coli.  
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;  
OC Enterobacteriaceae; Escherichia.  
OX NCBI\_TaxID=562;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=pRJ1004;  
RX MEDLINE=96130847; PubMed=8594334;  
RA Brown N.L., Barrett S.R., Camakaris J., Lee B.T., Rouch D.A.;  
RT "Molecular genetics and transport analysis of the copper-resistance  
RT determinants (pco) from Escherichia coli plasmid pRJ1004."  
RL Mol. Microbiol. 17:1153-1166(1995).  
DR EMBL; X83541; CAA58524.1; -.  
DR PIR; S70166; S52252.  
FT NON\_TER 11 11  
SQ SEQUENCE 11 AA; 1195 MW; 47D864F8ADC1A057 CRC64;

Query Match 18.2%; Score 2; DB 2; Length 11;  
Best Local Similarity 100.0%; Pred. No. 1.2e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 TA 9  
||  
Db 6 TA 7

RESULT 4

Q9AIZ7

ID Q9AIZ7 PRELIMINARY; PRT; 11 AA.  
AC Q9AIZ7;  
DT 01-JUN-2001 (TrEMBLrel. 17, Created)  
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)  
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)  
DE Tryptophanyl-tRNA synthetase (Fragment).  
GN TRPS.  
OS Carsonella ruddii.  
OC Bacteria; Proteobacteria; Gammaproteobacteria; Candidatus Carsonella.  
OX NCBI\_TaxID=114186;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=20336438; PubMed=10877784;  
RA Thao M.L., Moran N.A., Abbot P., Brennan E.B., Burckhardt D.H.,  
RA Baumann P.;

RT "Cospeciation of psyllids and their primary prokaryotic  
 RT endosymbionts.";  
 RL Appl. Environ. Microbiol. 66:2898-2905(2000).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=21125546; PubMed=11222582;  
 RA Clark M.A., Baumann L., Thao M.L., Moran N.A., Baumann P.;  
 RT "Degenerative Minimalism in the Genome of a Psyllid Endosymbiont.";  
 RL J. Bacteriol. 183:1853-1861(2001).  
 DR EMBL; AF211132; AAK15377.1; -.  
 DR GO; GO:0004812; F:tRNA ligase activity; IEA.  
 KW Aminoacyl-tRNA synthetase.  
 FT NON\_TER 1 1  
 SQ SEQUENCE 11 AA; 1333 MW; A28C67D6533059C6 CRC64;

Query Match 18.2%; Score 2; DB 2; Length 11;  
 Best Local Similarity 100.0%; Pred. No. 1.2e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 10 IK 11  
 ||  
 Db 6 IK 7

# RESULT 5

Q8RKN1

ID Q8RKN1 PRELIMINARY; PRT; 11 AA.  
 AC Q8RKN1;  
 DT 01-JUN-2002 (TrEMBLrel. 21, Created)  
 DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)  
 DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)  
 DE Beta-lactamase CTX-M-9 (Fragment).  
 GN BLACTX-M-9.  
 OS Escherichia coli.  
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;  
 OC Enterobacteriaceae; Escherichia.  
 OX NCBI\_TaxID=562;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=743-D;  
 RA Sabate M., Navarro F., Miro E., Campoy S., Mirelis B., Barbe J.,  
 RA Prats G.;  
 RT "A novel complex sull-type integron in Escherichia coli carrying the  
 RT bla(CTX-M-9) gene.";  
 RL Submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases.  
 DR EMBL; AY092058; AAM15718.1; -.  
 FT NON\_TER 1 1  
 SQ SEQUENCE 11 AA; 1071 MW; C26BF418D050440D CRC64;

Query Match 18.2%; Score 2; DB 2; Length 11;  
 Best Local Similarity 100.0%; Pred. No. 1.2e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AR 2  
 ||  
 Db 4 AR 5

RESULT 6

Q8L2T4

ID Q8L2T4 PRELIMINARY; PRT; 11 AA.  
 AC Q8L2T4;  
 DT 01-OCT-2002 (TrEMBLrel. 22, Created)  
 DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)  
 DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)  
 DE Histidinol phosphatase (Fragment).  
 OS Neisseria meningitidis.  
 OC Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;  
 OC Neisseriaceae; Neisseria.  
 OX NCBI\_TaxID=487;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=126E;  
 RX MEDLINE=22051050; PubMed=12055303;  
 RA Zhu P., Klutch M.J., Bash M.C., Tsang R.S.W., Ng L.K., Tsai C.M.;  
 RT "Genetic Diversity of Three Lgt Loci for Biosynthesis of  
 RT Lipooligosaccharide (LOS) in Neisseria Species."  
 RL Microbiology 148:1833-1844(2002).  
 DR EMBL; AF470685; AAM33538.1; -.  
 FT NON\_TER 11 11  
 SQ SEQUENCE 11 AA; 1273 MW; 01EC828D0AA72050 CRC64;

Query Match 18.2%; Score 2; DB 2; Length 11;  
 Best Local Similarity 100.0%; Pred. No. 1.2e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 RD 6  
 ||  
 Db 8 RD 9

RESULT 7

P77404

ID P77404 PRELIMINARY; PRT; 11 AA.  
 AC P77404;  
 DT 01-FEB-1997 (TrEMBLrel. 02, Created)  
 DT 01-FEB-1997 (TrEMBLrel. 02, Last sequence update)  
 DT 01-NOV-1998 (TrEMBLrel. 08, Last annotation update)  
 DE DNA sequence downstream of the ECOPRRI HSD locus (Fragment).  
 GN HSDR.  
 OS Escherichia coli.  
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;  
 OC Enterobacteriaceae; Escherichia.  
 OX NCBI\_TaxID=562;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=97206151; PubMed=9157244;  
 RA Tyndall C., Lehnher H., Sandmeier U., Kulik E., Bickle T.A.;  
 RT "The type IC hsd loci of the enterobacteria are flanked by DNA with  
 RT high homology to the phage P1 genome: implications for the evolution  
 RT and spread of DNA restriction systems."  
 RL Mol. Microbiol. 23:729-736(1997).  
 DR EMBL; X98145; CAA66840.1; -.  
 DR EMBL; X98144; CAA66839.1; -.



FT NON\_TER 1 1  
SQ SEQUENCE 11 AA; 1259 MW; 714AB092A4072734 CRC64;

Query Match 18.2%; Score 2; DB 2; Length 11;  
Best Local Similarity 100.0%; Pred. No. 1.2e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 KS 4  
||  
Db 1 KS 2

RESULT 8

Q8RMI8

ID Q8RMI8 PRELIMINARY; PRT; 11 AA.  
AC Q8RMI8;  
DT 01-JUN-2002 (TrEMBLrel. 21, Created)  
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)  
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)  
DE ErmB (Fragment).  
GN ERMB.  
OS Enterococcus hirae.  
OG Plasmid pMKH1.  
OC Bacteria; Firmicutes; Lactobacillales; Enterococcaceae; Enterococcus.  
OX NCBI\_TaxID=1354;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Borgen K., Sorum M., Wasteson Y., Kruse H., Oppegaard H.;  
RT "Genetic linkage between ermB and vanA in Enterococcus hirae of  
RT poultry origin."  
RL Submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases.  
DR EMBL; AF493942; AAM18554.1; -.  
DR GO; GO:0046821; C:extrachromosomal DNA; IEA.  
KW Plasmid.  
FT NON\_TER 1 1  
SQ SEQUENCE 11 AA; 1359 MW; 08A7A8AA49C7273B CRC64;

Query Match 18.2%; Score 2; DB 2; Length 11;  
Best Local Similarity 100.0%; Pred. No. 1.2e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 RK 3  
||  
Db 10 RK 11

RESULT 9

Q44090

ID Q44090 PRELIMINARY; PRT; 11 AA.  
AC Q44090;  
DT 01-NOV-1996 (TrEMBLrel. 01, Created)  
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)  
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)  
DE Hypothetical export segment (Fragment).  
OS Acholeplasma laidlawii.  
OC Bacteria; Firmicutes; Mollicutes; Acholeplasmatales;  
OC Acholeplasmataceae; Acholeplasma.

OX NCBI\_TaxID=2148;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=A-EF22;  
 RA Boyer M.J., Jarhede T.K., Tegman V., Wieslander A.;  
 RT "Sequence regions from *Acholeplasma laidlawii* which restore export of  
 RT beta-lactamase in *Escherichia coli*.";  
 RL Submitted (JUN-1993) to the EMBL/GenBank/DDBJ databases.  
 DR EMBL; Z22875; CAA80495.1; -.  
 DR PIR; S33519; S33519.  
 FT NON\_TER 11 11  
 SQ SEQUENCE 11 AA; 1234 MW; 5C9D2AE8A682C337 CRC64;

Query Match 18.2%; Score 2; DB 2; Length 11;  
 Best Local Similarity 100.0%; Pred. No. 1.2e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 MT 8  
 ||  
 Db 7 MT 8

RESULT 10  
 Q44237

ID Q44237 PRELIMINARY; PRT; 11 AA.  
 AC Q44237;  
 DT 01-NOV-1996 (TrEMBLrel. 01, Created)  
 DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)  
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)  
 DE Glutamine synthetase (Fragment).  
 GN GLNA.  
 OS *Anabaena* sp. (strain PCC 7120).  
 OC Bacteria; Cyanobacteria; Nostocales; Nostocaceae; Nostoc.  
 OX NCBI\_TaxID=103690;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=PCC 7120;  
 RA Warner L.E., Ligon P.J., Stahel A.W., Curtis S.E.;  
 RT "The *apcF* gene of *Anabaena* sp. strain PCC 7120 is regulated by  
 RT nitrogen and the *apcF* and *glnA* promoters overlap.";  
 RL Submitted (MAY-1995) to the EMBL/GenBank/DDBJ databases.  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=PCC 7120;  
 RA Scappino L.A.;  
 RL Submitted (FEB-1995) to the EMBL/GenBank/DDBJ databases.  
 DR EMBL; U21853; AAA65652.1; -.  
 FT NON\_TER 11 11  
 SQ SEQUENCE 11 AA; 1316 MW; 2000580E32CB06C7 CRC64;

Query Match 18.2%; Score 2; DB 2; Length 11;  
 Best Local Similarity 100.0%; Pred. No. 1.2e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 MT 8  
 ||  
 Db 1 MT 2

RESULT 11

Q9R872

ID Q9R872 PRELIMINARY; PRT; 11 AA.  
 AC Q9R872;  
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)  
 DE Dihydrofolate reductase (Fragment).  
 GN DFR1.  
 OS Escherichia coli.  
 OG Plasmid r483.  
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;  
 OC Enterobacteriaceae; Escherichia.  
 OX NCBI\_TaxID=562;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TRANSPOSON=Tn7;  
 RA Hansson K., Sundstrom L., Pelletier A., Roy P.H.;  
 RT "Sequence and function of the second type of integron in Tn7."  
 RL Submitted (SEP-1997) to the EMBL/GenBank/DDBJ databases.  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC TRANSPOSON=Tn7;  
 RX MEDLINE=82220022; PubMed=6283361;  
 RA Lichtenstein C., Brenner S.;  
 RT "Unique insertion site of Tn7 in the E. coli chromosome."  
 RL Nature 297:601-603(1982).  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RC TRANSPOSON=Tn7;  
 RX MEDLINE=83290694; PubMed=6411680;  
 RA Simonsen C.C., Chen E.Y., Levinson A.D.;  
 RT "Identification of the type I trimethoprim-resistant dihydrofolate  
 RT reductase specified by the Escherichia coli R-plasmid R483: Comparison  
 RT with procaryotic and eucaryotic dihydrofolate reductases."  
 RL J. Bacteriol. 155:1001-1008(1983).  
 RN [4]  
 RP SEQUENCE FROM N.A.  
 RC TRANSPOSON=Tn7;  
 RX MEDLINE=83272957; PubMed=6308574;  
 RA Fling M.E., Richards C.;  
 RT "The nucleotide sequence of the trimethoprim-resistant dihydrofolate  
 RT reductase gene harbored by Tn7."  
 RL Nucleic Acids Res. 11:5147-5158(1983).  
 DR EMBL; AJ001816; CAA05032.1; -.  
 DR GO; GO:0046821; C:extrachromosomal DNA; IEA.  
 KW Plasmid.  
 FT NON\_TER 11 11  
 SQ SEQUENCE 11 AA; 1221 MW; 92014864C2C69735 CRC64;

Query Match 18.2%; Score 2; DB 2; Length 11;  
 Best Local Similarity 100.0%; Pred. No. 1.2e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db                    ||  
                      8 AI 9

RESULT 12

Q8GL24

ID    Q8GL24            PRELIMINARY;            PRT;        11 AA.  
AC    Q8GL24;  
DT    01-MAR-2003 (TrEMBLrel. 23, Created)  
DT    01-MAR-2003 (TrEMBLrel. 23, Last sequence update)  
DT    01-JUN-2003 (TrEMBLrel. 24, Last annotation update)  
DE    PF-50 protein (Fragment).  
GN    PF-50.  
OS    Borrelia burgdorferi (Lyme disease spirochete).  
OG    Plasmid group cp32-6.  
OC    Bacteria; Spirochaetes; Spirochaetales; Spirochaetaceae; Borrelia.  
OX    NCBI\_TaxID=139;  
RN    [1]  
RP    SEQUENCE FROM N.A.  
RC    STRAIN=Sh-2-82;  
RA    Stevenson B., Miller J.C.;  
RT    "Comparative analyses of Borrelia burgdorferi erp genes and their cp32  
RT    prophages: conservation amidst diversity."  
RL    Submitted (AUG-2002) to the EMBL/GenBank/DDBJ databases.  
DR    EMBL; AY142093; AAN17876.1; -.  
DR    GO; GO:0046821; C:extrachromosomal DNA; IEA.  
KW    Plasmid.  
FT    NON\_TER            1            1  
SQ    SEQUENCE    11 AA;    1366 MW;    4E441D5330504373 CRC64;

Query Match                    18.2%;    Score 2;    DB 2;    Length 11;  
Best Local Similarity    100.0%;    Pred. No. 1.2e+05;  
Matches        2;    Conservative        0;    Mismatches        0;    Indels        0;    Gaps        0;

Qy                    10 IK 11  
                      ||  
Db                    3 IK 4

RESULT 13

Q8GL19

ID    Q8GL19            PRELIMINARY;            PRT;        11 AA.  
AC    Q8GL19;  
DT    01-MAR-2003 (TrEMBLrel. 23, Created)  
DT    01-MAR-2003 (TrEMBLrel. 23, Last sequence update)  
DT    01-JUN-2003 (TrEMBLrel. 24, Last annotation update)  
DE    PF-50 protein (Fragment).  
GN    PF-50.  
OS    Borrelia burgdorferi (Lyme disease spirochete).  
OG    Plasmid group cp32-11.  
OC    Bacteria; Spirochaetes; Spirochaetales; Spirochaetaceae; Borrelia.  
OX    NCBI\_TaxID=139;  
RN    [1]  
RP    SEQUENCE FROM N.A.  
RC    STRAIN=Sh-2-82;  
RA    Stevenson B., Miller J.C.;  
RT    "Comparative analyses of Borrelia burgdorferi erp genes and their cp32

RT prophages: conservation amidst diversity.";  
 RL Submitted (AUG-2002) to the EMBL/GenBank/DDBJ databases.  
 DR EMBL; AY142096; AAN17880.1; -.  
 DR GO; GO:0046821; C:extrachromosomal DNA; IEA.  
 KW Plasmid.  
 FT NON\_TER 1 1  
 SQ SEQUENCE 11 AA; 1366 MW; 4E441D5337204373 CRC64;

Query Match 18.2%; Score 2; DB 2; Length 11;  
 Best Local Similarity 100.0%; Pred. No. 1.2e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 IK 11  
 ||  
 Db 3 IK 4

#### RESULT 14

Q7WUL8

ID Q7WUL8 PRELIMINARY; PRT; 11 AA.  
 AC Q7WUL8;  
 DT 01-OCT-2003 (TrEMBLrel. 25, Created)  
 DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)  
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
 DE PdtJ (Fragment).  
 GN PDTJ.  
 OS Pseudomonas putida.  
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;  
 OC Pseudomonadaceae; Pseudomonas.  
 OX NCBI\_TaxID=303;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=DSM 3601;  
 RA Lewis T.A., Leach L., Morales S.E., Austin P.R., Hartwell H.J.,  
 RA Kaplan B., Forker C., Meyer J.-M.;  
 RT "Physiological and molecular genetic evaluation of the dechlorination  
 RT agent, pyridine-2,6-bis (monothiocarboxylic acid) (PDTC), as a  
 RT secondary siderophore of Pseudomonas sp.";  
 RL Submitted (JUN-2003) to the EMBL/GenBank/DDBJ databases.  
 DR EMBL; AY319946; AAQ01713.1; -.  
 FT NON\_TER 11 11  
 SQ SEQUENCE 11 AA; 1143 MW; C22A6E13A050587D CRC64;

Query Match 18.2%; Score 2; DB 2; Length 11;  
 Best Local Similarity 100.0%; Pred. No. 1.2e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 TA 9  
 ||  
 Db 3 TA 4

#### RESULT 15

Q9URG1

ID Q9URG1 PRELIMINARY; PRT; 11 AA.  
 AC Q9URG1;  
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)

DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
 DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)  
 DE Cytochrome C oxidase subunit 2 (Fragment).  
 OS Neurospora crassa.  
 OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;  
 OC Sordariomycetidae; Sordariales; Sordariaceae; Neurospora.  
 OX NCBI\_TaxID=5141;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=92035058; PubMed=1657411;  
 RA Lemire E.G., Percy J.A., Correia J.M., Crowther B.M., Nargang F.E.;  
 RT "Alteration of the cytochrome c oxidase subunit 2 gene in the [exn-5]  
 RT mutant of Neurospora crassa."  
 RL Curr. Genet. 20:121-127(1991).  
 FT NON\_TER 1 1  
 FT NON\_TER 11 11  
 SQ SEQUENCE 11 AA; 1222 MW; 936B1558C7605DC5 CRC64;

Query Match 18.2%; Score 2; DB 3; Length 11;  
 Best Local Similarity 100.0%; Pred. No. 1.2e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 AI 10  
 ||  
 Db 5 AI 6

#### RESULT 16

Q96V15

ID Q96V15 PRELIMINARY; PRT; 11 AA.  
 AC Q96V15;  
 DT 01-DEC-2001 (TrEMBLrel. 19, Created)  
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)  
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)  
 DE Pheromone alpha (Fragment).  
 GN MFALPHA1A.  
 OS Cryptococcus neoformans var. neoformans.  
 OC Eukaryota; Fungi; Basidiomycota; Hymenomycetes; Heterobasidiomycetes;  
 OC Tremellomycetidae; Tremellales; Tremellaceae; Filobasidiella.  
 OX NCBI\_TaxID=40410;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=IUM 98-3351;  
 RX MEDLINE=21538945; PubMed=11682503;  
 RA Cogliati M., Esposto M.C., Clarke D.L., Wickes B.L., Viviani M.A.;  
 RT "Origin of Cryptococcus neoformans var. neoformans Diploid Strains."  
 RL J. Clin. Microbiol. 39:3889-3894(2001).  
 DR EMBL; AF377019; AAK55615.1; -.  
 FT NON\_TER 1 1  
 FT NON\_TER 11 11  
 SQ SEQUENCE 11 AA; 1154 MW; C764AF6E786761ED CRC64;

Query Match 18.2%; Score 2; DB 3; Length 11;  
 Best Local Similarity 100.0%; Pred. No. 1.2e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 MT 8

Db                    ||  
                      9 MT 10

RESULT 17

Q14759

ID    Q14759            PRELIMINARY;            PRT;        11 AA.  
AC    Q14759;  
DT    01-NOV-1996 (TrEMBLrel. 01, Created)  
DT    01-NOV-1996 (TrEMBLrel. 01, Last sequence update)  
DT    01-DEC-2001 (TrEMBLrel. 19, Last annotation update)  
DE    Lymphocyte cytosolic protein 2 (Fragment).  
GN    LCP2.  
OS    Homo sapiens (Human).  
OC    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC    Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX    NCBI\_TaxID=9606;  
RN    [1]  
RP    SEQUENCE FROM N.A.  
RA    Sunden S.L.F., Carr L.L., Clements J.L., Motto D.G., Koretzky G.A.;  
RT    "Polymorphism in and localization of the gene encoding the 76 kDa SH2  
RT    domain-containing Leukocyte Protein (SLP-76) to chromosome 5q33.1-  
RT    qter.";  
RL    Genomics 0:0-0(1995).  
DR    EMBL; U44065; AAA93308.1; -.  
FT    NON\_TER            1            1  
FT    NON\_TER            11           11  
SQ    SEQUENCE    11 AA;    1242 MW;    D695104224072DDD CRC64;

Query Match                    18.2%;    Score 2;    DB 4;    Length 11;  
Best Local Similarity        100.0%;    Pred. No. 1.2e+05;  
Matches        2;    Conservative        0;    Mismatches        0;    Indels        0;    Gaps        0;

Qy                    2 RK 3  
                      ||  
Db                    7 RK 8

RESULT 18

Q9NY38

ID    Q9NY38            PRELIMINARY;            PRT;        11 AA.  
AC    Q9NY38;  
DT    01-OCT-2000 (TrEMBLrel. 15, Created)  
DT    01-OCT-2000 (TrEMBLrel. 15, Last sequence update)  
DT    01-OCT-2000 (TrEMBLrel. 15, Last annotation update)  
DE    Heavy metal-responsive transcription factor (Fragment).  
GN    MTF-1.  
OS    Homo sapiens (Human).  
OC    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC    Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX    NCBI\_TaxID=9606;  
RN    [1]  
RP    SEQUENCE FROM N.A.  
RA    Auf der Maur A., Belser T., Wang Y., Gunes C., Lichtlen P.,  
RA    Georgiev O., Schaffner W.;  
RT    "Characterization of the mouse gene for the heavy metal-responsive  
RT    transcription factor MTF-1.";

RL Submitted (DEC-1999) to the EMBL/GenBank/DDBJ databases.  
 DR EMBL; AJ251881; CAB71327.1; -.  
 FT NON\_TER 1 1  
 FT NON\_TER 11 11  
 SQ SEQUENCE 11 AA; 1099 MW; A8653693773772C6 CRC64;

Query Match 18.2%; Score 2; DB 4; Length 11;  
 Best Local Similarity 100.0%; Pred. No. 1.2e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 AI 10  
 ||  
 Db 2 AI 3

# RESULT 19

Q9Y3G2

ID Q9Y3G2 PRELIMINARY; PRT; 11 AA.  
 AC Q9Y3G2;  
 DT 01-NOV-1999 (TrEMBLrel. 12, Created)  
 DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)  
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)  
 DE LSFR2 protein (Fragment).  
 GN LSFR2.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=99299247; PubMed=10369878;  
 RA Gilley J., Fried M.;  
 RT "Extensive gene order differences within regions of conserved synten  
 RT between the Fugu and human genomes: implications for chromosomal  
 RT volution and the cloning of disease genes."  
 RL Hum. Mol. Genet. 8:1313-1320(1999).  
 DR EMBL; Y17456; CAB44349.1; -.  
 FT NON\_TER 1 1  
 FT NON\_TER 11 11  
 SQ SEQUENCE 11 AA; 1342 MW; 68C5E5D7A8772324.CRC64;

Query Match 18.2%; Score 2; DB 4; Length 11;  
 Best Local Similarity 100.0%; Pred. No. 1.2e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 RK 3  
 ||  
 Db 4 RK 5

# RESULT 20

Q9UNL8

ID Q9UNL8 PRELIMINARY; PRT; 11 AA.  
 AC Q9UNL8;  
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
 DT 01-MAY-2000 (TrEMBLrel. 13, Last annotation update)



DE APC2 protein (Fragment).  
 GN APC2.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Carr I.M., Markham A.F., Colleta P.L., Wai L., Askham J., Morrison E.,  
 RA Meredith D.M.;  
 RT "APC2 partial gene sequence."  
 RL Submitted (DEC-1998) to the EMBL/GenBank/DDBJ databases.  
 DR EMBL; AF110338; AAD29275.1; -.  
 FT NON\_TER 1 1  
 FT NON\_TER 11 11  
 SQ SEQUENCE 11 AA; 1326 MW; 75881D7BB441EAB4 CRC64;

Query Match 18.2%; Score 2; DB 4; Length 11;  
 Best Local Similarity 100.0%; Pred. No. 1.2e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 RD 6  
 ||  
 Db 4 RD 5

# RESULT 21

Q9UCP5

ID Q9UCP5 PRELIMINARY; PRT; 11 AA.  
 AC Q9UCP5;  
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)  
 DE AggreCAN core protein (Fragment).  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE.  
 RX MEDLINE=92235266; PubMed=1569188;  
 RA Sandy J.D., Flannery C.R., Neame P.J., Lohmander L.S.;  
 RL J. Clin. Invest. 89:1512-1516(1992).  
 DR GO; GO:0005201; F:extracellular matrix structural constituent; TAS.  
 DR GO; GO:0006508; P:proteolysis and peptidolysis; NAS.  
 DR GO; GO:0001501; P:skeletal development; NAS.  
 FT NON\_TER 1 1  
 FT NON\_TER 11 11  
 SQ SEQUENCE 11 AA; 1149 MW; 8FBFE8DFE72042D5 CRC64;

Query Match 18.2%; Score 2; DB 4; Length 11;  
 Best Local Similarity 100.0%; Pred. No. 1.2e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AR 2  
 ||  
 Db 1 AR 2

RESULT 22

Q16234

ID Q16234 PRELIMINARY; PRT; 11 AA.  
 AC Q16234;  
 DT 01-NOV-1996 (TrEMBLrel. 01, Created)  
 DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)  
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)  
 DE HuD protein (Fragment).  
 GN HUD.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=94349312; PubMed=8069866;  
 RA Sekido Y., Bader S.A., Carbone D.P., Johnson B.E., Minna J.D.;  
 RT "Molecular analysis of the HuD gene encoding a paraneoplastic  
 RT encephalomyelitis antigen in human lung cancer cell lines."  
 RL Cancer Res. 54:4988-4992(1994).  
 DR EMBL; S73887; AAD14142.1; -.  
 DR PIR; I52708; I52708.  
 FT NON\_TER 11 11  
 SQ SEQUENCE 11 AA; 1289 MW; 2EDCF20E204415A7 CRC64;

Query Match 18.2%; Score 2; DB 4; Length 11;  
 Best Local Similarity 100.0%; Pred. No. 1.2e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 SR 5  
 ||  
 Db 5 SR 6

RESULT 23

Q9UBM2

ID Q9UBM2 PRELIMINARY; PRT; 11 AA.  
 AC Q9UBM2;  
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)  
 DE ETV6 protein (Fragment).  
 GN ETV6.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Montgomery K.T., Lau S.T., Renault B., Yoon S.J., Baens M.,  
 RA Marynen P., Kucherlapati R.;  
 RT "Towards the Complete Sequence of Chromosome 12."  
 RL Submitted (DEC-1996) to the EMBL/GenBank/DDBJ databases.  
 RN [2]  
 RP SEQUENCE FROM N.A.

RA Baens M., Peeters P., Guo C., Aerssens J., Marynen P.;  
RL Submitted (JAN-1996) to the EMBL/GenBank/DDBJ databases.  
DR EMBL; U81830; AAB39862.1; -.  
DR EMBL; U45432; AAB17016.1; -.  
FT NON\_TER 11 11  
SQ SEQUENCE 11 AA; 1194 MW; 8267C587A6DDC771 CRC64;

Query Match 18.2%; Score 2; DB 4; Length 11;  
Best Local Similarity 100.0%; Pred. No. 1.2e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 10 IK 11  
||  
Db 10 IK 11

RESULT 24

Q8NI03

ID Q8NI03 PRELIMINARY; PRT; 11 AA.  
AC Q8NI03;  
DT 01-OCT-2002 (TrEMBLrel. 22, Created)  
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)  
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)  
DE 25 hydroxyvitamin d3 1-alpha hydroxylase (Fragment).  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Ebert R., Schneider D., Jovanovic M., Adamski J., Jakob F.;  
RL Submitted (APR-2002) to the EMBL/GenBank/DDBJ databases.  
DR EMBL; AF500480; AAM21669.1; -.  
FT NON\_TER 11 11  
SQ SEQUENCE 11 AA; 1298 MW; 82C14E84CB533731 CRC64;

Query Match 18.2%; Score 2; DB 4; Length 11;  
Best Local Similarity 100.0%; Pred. No. 1.2e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 SR 5  
||  
Db 9 SR 10

RESULT 25

Q9UCR1

ID Q9UCR1 PRELIMINARY; PRT; 11 AA.  
AC Q9UCR1;  
DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)  
DE AUTOTAXIN (Fragment).  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;

RN [1]  
 RP SEQUENCE.  
 RX MEDLINE=92129337; PubMed=1733949;  
 RA Stracke M.L., Krutzsch H.C., Unsworth E.J., Arestad A., Cioce V.,  
 RA Schiffmann E., Liotta L.A.;  
 RT "Identification, purification, and partial sequence analysis of  
 RT autotaxin, a novel motility-stimulating protein.";  
 RL J. Biol. Chem. 267:2524-2529(1992).  
 FT NON\_TER 1 1  
 FT NON\_TER 11 11  
 SQ SEQUENCE 11 AA; 1171 MW; 2723615AA0437737 CRC64;

Query Match 18.2%; Score 2; DB 4; Length 11;  
 Best Local Similarity 100.0%; Pred. No. 1.2e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 TA 9  
 ||  
 Db 8 TA 9

# RESULT 26

## Q9HCN5

ID Q9HCN5 PRELIMINARY; PRT; 11 AA.  
 AC Q9HCN5;  
 DT 01-MAR-2001 (TrEMBLrel. 16, Created)  
 DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)  
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)  
 DE Platelet glycoprotein VI (Fragment).  
 GN GPVI OR GP6.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=20483673; PubMed=11027634;  
 RA Ezumi Y., Uchiyama T., Takayama H.;  
 RT "Molecular cloning, genomic structure, chromosomal localization, and  
 RT alternative splice forms of the platelet collagen receptor  
 RT glycoprotein VI.";  
 RL Biochem. Biophys. Res. Commun. 277:27-36(2000).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=22359008; PubMed=12359731;  
 RA Holmes M.L., Bartle N., Eisbacher M., Chong B.H.;  
 RT "Cloning and Analysis of the Thrombopoietin-induced Megakaryocyte-  
 RT specific Glycoprotein VI Promoter and Its Regulation by GATA-1, Fli-1,  
 RT and Spl.";  
 RL J. Biol. Chem. 277:48333-48341(2002).  
 DR EMBL; AB043943; BAB12248.1; -.  
 DR EMBL; AF521646; AAN86273.1; -.  
 FT NON\_TER 11 11  
 SQ SEQUENCE 11 AA; 1166 MW; 8D7839FE2DC1B775 CRC64;

Query Match 18.2%; Score 2; DB 4; Length 11;  
 Best Local Similarity 100.0%; Pred. No. 1.2e+05;

Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 TA 9  
 ||  
 Db 6 TA 7

RESULT 27

Q25916

ID Q25916 PRELIMINARY; PRT; 11 AA.  
 AC Q25916;  
 DT 01-NOV-1996 (TrEMBLrel. 01, Created)  
 DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)  
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)  
 DE Malaria antigen (7H8/2) (Fragment).  
 OS Plasmodium falciparum.  
 OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.  
 OX NCBI\_TaxID=5833;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=91164876; PubMed=1706114;  
 RA Limpaboon T., Taylor D., Jones G., Geysen H.M., Saul A.;  
 RT "Characterization of a Plasmodium falciparum epitope recognized by a  
 RT monoclonal antibody with broad isolate and species specificity.";  
 RL Southeast Asian J. Trop. Med. Public Health 21:388-396(1990).  
 DR EMBL; M31305; AAA29645.1; -.  
 FT NON\_TER 1 1  
 SQ SEQUENCE 11 AA; 1415 MW; DB03D3BC42C33699 CRC64;

Query Match 18.2%; Score 2; DB 5; Length 11;  
 Best Local Similarity 100.0%; Pred. No. 1.2e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 KS 4  
 ||  
 Db 1 KS 2

RESULT 28

Q9NFX0

ID Q9NFX0 PRELIMINARY; PRT; 11 AA.  
 AC Q9NFX0;  
 DT 01-OCT-2000 (TrEMBLrel. 15, Created)  
 DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)  
 DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)  
 DE Mitochondrial aconitase (Fragment).  
 GN ACON OR MAC OR CG9244.  
 OS Drosophila melanogaster (Fruit fly).  
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
 OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;  
 OC Ephydroidea; Drosophilidae; Drosophila.  
 OX NCBI\_TaxID=7227;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=CANTON S;  
 RA Lind M.I.;  
 RT "Charaterisation of two iron regulatory proteins and mitochondrial

RT aconitase in *Drosophila melanogaster*.";  
RL Submitted (DEC-1999) to the EMBL/GenBank/DDBJ databases.  
DR EMBL; AJ252019; CAB93522.1; -.  
DR FlyBase; FBgn0010100; Acon.  
FT NON\_TER 11 11  
SQ SEQUENCE 11 AA; 1204 MW; 7C889CE4D4469734 CRC64;

Query Match 18.2%; Score 2; DB 5; Length 11;  
Best Local Similarity 100.0%; Pred. No. 1.2e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AR 2  
11  
Db 3 AR 4

RESULT 29

Q8MPQ3

ID Q8MPQ3 PRELIMINARY; PRT; 11 AA.  
AC Q8MPQ3;  
DT 01-OCT-2002 (TrEMBLrel. 22, Created)  
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)  
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)  
DE Hypothetical protein Y23H5A.8b.  
GN Y23H5A.8.  
OS *Caenorhabditis elegans*.  
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;  
OC Rhabditidae; Peloderinae; *Caenorhabditis*.  
OX NCBI\_TaxID=6239;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=Bristol N2;  
RX MEDLINE=99069613; PubMed=9851916;  
RA Waterston R.;  
RT "Genome sequence of the nematode *C. elegans*: a platform for  
RT investigating biology. The *C. elegans* Sequencing Consortium."  
RL Science 282:2012-2018(1998).  
RN [2]  
RP SEQUENCE FROM N.A.  
RC STRAIN=Bristol N2;  
RA Dempsey S., Le T.T.;  
RT "The sequence of *C. elegans* cosmid Y23H5A.";  
RL Submitted (JUL-1998) to the EMBL/GenBank/DDBJ databases.  
RN [3]  
RP SEQUENCE FROM N.A.  
RC STRAIN=Bristol N2;  
RA Waterston R.;  
RL Submitted (JUN-2002) to the EMBL/GenBank/DDBJ databases.  
DR EMBL; AF077541; AAM54173.1; -.  
DR WormPep; Y23H5A.8b; CE31097.  
KW Hypothetical protein.  
SQ SEQUENCE 11 AA; 1319 MW; 6920D63A21B77414 CRC64;

Query Match 18.2%; Score 2; DB 5; Length 11;  
Best Local Similarity 100.0%; Pred. No. 1.2e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 SR 5  
||  
Db 3 SR 4

RESULT 30

Q9TRR7

ID Q9TRR7 PRELIMINARY; PRT; 11 AA.  
AC Q9TRR7;  
DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)  
DE Calcyclin-associated protein, CAP50=CA2+/phospholipid-binding protein  
DE L-13 fragment (Fragment).  
OS *Oryctolagus cuniculus* (Rabbit).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Lagomorpha; Leporidae; *Oryctolagus*.  
OX NCBI\_TaxID=9986;  
RN [1]  
RP SEQUENCE.  
RX MEDLINE=92250478; PubMed=1533622;  
RA Tokumitsu H., Mizutani A., Minami H., Kobayashi R., Hidaka H.;  
RT "A calcyclin-associated protein is a newly identified member of the  
RT Ca2+/phospholipid-binding proteins, annexin family.";  
RL J. Biol. Chem. 267:8919-8924(1992).  
FT NON\_TER 1 1  
FT NON\_TER 11 11  
SQ SEQUENCE 11 AA; 1310 MW; 55580B0F5DDAA9C7 CRC64;

Query Match 18.2%; Score 2; DB 6; Length 11;  
Best Local Similarity 100.0%; Pred. No. 1.2e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 10 IK 11  
||  
Db 10 IK 11

RESULT 31

Q9XSP7

ID Q9XSP7 PRELIMINARY; PRT; 11 AA.  
AC Q9XSP7;  
DT 01-NOV-1999 (TrEMBLrel. 12, Created)  
DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)  
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)  
DE Platelet-derived growth factor A chain (Fragment).  
GN PDGFA.  
OS *Pygathrix nemaeus* (Dove langur).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae; Colobinae;  
OC *Pygathrix*.  
OX NCBI\_TaxID=54133;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=20065871; PubMed=10598812;  
RA Bonthron D.T., Smith S.L., Campbell R.;  
RT "Complex patterns of intragenic polymorphism at the PDGFA locus.";

RL Hum. Genet. 105:452-459(1999).  
 DR EMBL; AJ243282; CAB45924.1; -.  
 FT NON\_TER 1 1  
 FT NON\_TER 11 11  
 SQ SEQUENCE 11 AA; 1345 MW; 7FB881F101E1E044 CRC64;

Query Match 18.2%; Score 2; DB 6; Length 11;  
 Best Local Similarity 100.0%; Pred. No. 1.2e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 SR 5  
 ||  
 Db 3 SR 4

# RESULT 32

## Q9XSP2

ID Q9XSP2 PRELIMINARY; PRT; 11 AA.  
 AC Q9XSP2;  
 DT 01-NOV-1999 (TrEMBLrel. 12, Created)  
 DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)  
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)  
 DE Platelet-derived growth factor A chain (Fragment).  
 GN PDGFA.  
 OS Hylobates syndactylus (Siamang) (Symphalangus syndactylus).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hylobatidae; Hylobates.  
 OX NCBI\_TaxID=9590;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=20065871; PubMed=10598812;  
 RA Bonthron D.T., Smith S.L., Campbell R.;  
 RT "Complex patterns of intragenic polymorphism at the PDGFA locus."  
 RL Hum. Genet. 105:452-459(1999).  
 DR EMBL; AJ243280; CAB45927.1; -.  
 FT NON\_TER 1 1  
 FT NON\_TER 11 11  
 SQ SEQUENCE 11 AA; 1345 MW; 7FB881F101E1E044 CRC64;

Query Match 18.2%; Score 2; DB 6; Length 11;  
 Best Local Similarity 100.0%; Pred. No. 1.2e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 SR 5  
 ||  
 Db 3 SR 4

# RESULT 33

## Q9XSP5

ID Q9XSP5 PRELIMINARY; PRT; 11 AA.  
 AC Q9XSP5;  
 DT 01-NOV-1999 (TrEMBLrel. 12, Created)  
 DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)  
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)  
 DE Platelet-derived growth factor A chain (Fragment).  
 GN PDGFA.



OS Pan troglodytes (Chimpanzee).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.  
 OX NCBI\_TaxID=9598;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=20065871; PubMed=10598812;  
 RA Bonthron D.T., Smith S.L., Campbell R.;  
 RT "Complex patterns of intragenic polymorphism at the PDGFA locus."  
 RL Hum. Genet. 105:452-459(1999).  
 DR EMBL; AJ243277; CAB45926.1; -.  
 FT NON\_TER 1 1  
 FT NON\_TER 11 11  
 SQ SEQUENCE 11 AA; 1331 MW; 7FB881F101E1F2D4 CRC64;

Query Match 18.2%; Score 2; DB 6; Length 11;  
 Best Local Similarity 100.0%; Pred. No. 1.2e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 SR 5  
 ||  
 Db 3 SR 4

RESULT 34  
 Q9TQS9

ID Q9TQS9 PRELIMINARY; PRT; 11 AA.  
 AC Q9TQS9;  
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
 DT 01-MAY-2000 (TrEMBLrel. 13, Last annotation update)  
 DE Transferrin (Fragment).  
 OS Equus caballus (Horse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Perissodactyla; Equidae; Equus.  
 OX NCBI\_TaxID=9796;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Giffard J.M., Brandon R.B., Bell T.K.;  
 RT "Further identification of single nucleotide polymorphisms in the  
 RT equine transferrin gene."  
 RL Submitted (SEP-1999) to the EMBL/GenBank/DDBJ databases.  
 DR EMBL; AF185800; AAF05495.1; -.  
 DR EMBL; AF185797; AAF05492.1; -.  
 DR EMBL; AF185798; AAF05493.1; -.  
 DR EMBL; AF185799; AAF05494.1; -.  
 FT NON\_TER 11 11  
 SQ SEQUENCE 11 AA; 1231 MW; C586121E2DC4005D CRC64;

Query Match 18.2%; Score 2; DB 6; Length 11;  
 Best Local Similarity 100.0%; Pred. No. 1.2e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 AI 10  
 ||  
 Db 4 AI 5

RESULT 35

Q9TQS0

ID Q9TQS0 PRELIMINARY; PRT; 11 AA.  
 AC Q9TQS0;  
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
 DT 01-MAY-2000 (TrEMBLrel. 13, Last annotation update)  
 DE C-KIT (Fragment).  
 GN KIT.  
 OS Bos taurus (Bovine).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;  
 OC Bovidae; Bovinae; Bos.  
 OX NCBI\_TaxID=9913;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Olsen H.G., Vage D.I., Lien S., Klungland H.;  
 RT "A polymorphism in the bovine c-kit gene."  
 RL Submitted (JUN-1999) to the EMBL/GenBank/DDBJ databases.  
 DR EMBL; AJ243424; CAB60775.1; -.  
 DR EMBL; AJ243060; CAB60774.1; -.  
 FT NON\_TER 1 1  
 FT NON\_TER 11 11  
 SQ SEQUENCE 11 AA; 1126 MW; DD785FF8A2D2D772 CRC64;

Query Match 18.2%; Score 2; DB 6; Length 11;  
 Best Local Similarity 100.0%; Pred. No. 1.2e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 10 IK 11  
 ||  
 Db 1 IK 2

RESULT 36

Q9XSP8

ID Q9XSP8 PRELIMINARY; PRT; 11 AA.  
 AC Q9XSP8;  
 DT 01-NOV-1999 (TrEMBLrel. 12, Created)  
 DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)  
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)  
 DE Platelet-derived growth factor A chain (Fragment).  
 GN PDGFA.  
 OS Presbytis johnii.  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae; Colobinae;  
 OC Presbytis.  
 OX NCBI\_TaxID=98375;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=20065871; PubMed=10598812;  
 RA Bonthron D.T., Smith S.L., Campbell R.;  
 RT "Complex patterns of intragenic polymorphism at the PDGFA locus."  
 RL Hum. Genet. 105:452-459(1999).  
 DR EMBL; AJ243281; CAB46013.1; -.  
 FT NON\_TER 1 1

FT NON\_TER 11 11  
SQ SEQUENCE 11 AA; 1345 MW; 7FB881F101E1E044 CRC64;

Query Match 18.2%; Score 2; DB 6; Length 11;  
Best Local Similarity 100.0%; Pred. No. 1.2e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 SR 5  
||  
Db 3 SR 4

RESULT 37

Q9XSP6

ID Q9XSP6 PRELIMINARY; PRT; 11 AA.  
AC Q9XSP6;  
DT 01-NOV-1999 (TrEMBLrel. 12, Created)  
DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)  
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)  
DE Platelet-derived growth factor A chain (Fragment).  
GN PDGFA.  
OS Pongo pygmaeus (Orangutan).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pongo.  
OX NCBI\_TaxID=9600;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=20065871; PubMed=10598812;  
RA Bonthron D.T., Smith S.L., Campbell R.;  
RT "Complex patterns of intragenic polymorphism at the PDGFA locus."  
RL Hum. Genet. 105:452-459(1999).  
DR EMBL; AJ243279; CAB45925.1; -.  
FT NON\_TER 1 1  
FT NON\_TER 11 11  
SQ SEQUENCE 11 AA; 1345 MW; 7FB881F101E1E044 CRC64;

Query Match 18.2%; Score 2; DB 6; Length 11;  
Best Local Similarity 100.0%; Pred. No. 1.2e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 SR 5  
||  
Db 3 SR 4

RESULT 38

Q9XSQ4

ID Q9XSQ4 PRELIMINARY; PRT; 11 AA.  
AC Q9XSQ4;  
DT 01-NOV-1999 (TrEMBLrel. 12, Created)  
DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)  
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)  
DE Platelet-derived growth factor A chain (Fragment).  
GN PDGFA.  
OS Gorilla gorilla (gorilla).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Gorilla.

OX NCBI\_TaxID=9593;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=20065871; PubMed=10598812;  
 RA Bonthron D.T., Smith S.L., Campbell R.;  
 RT "Complex patterns of intragenic polymorphism at the PDGFA locus."  
 RL Hum. Genet. 105:452-459(1999).  
 DR EMBL; AJ243278; CAB45916.1; -.  
 FT NON\_TER 1 1  
 FT NON\_TER 11 11  
 SQ SEQUENCE 11 AA; 1331 MW; 7FB881F101E1F2D4 CRC64;

Query Match 18.2%; Score 2; DB 6; Length 11;  
 Best Local Similarity 100.0%; Pred. No. 1.2e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 SR 5  
 ||  
 Db 3 SR 4

# RESULT 39

O77900

ID O77900 PRELIMINARY; PRT; 11 AA.  
 AC O77900;  
 DT 01-NOV-1998 (TrEMBLrel. 08, Created)  
 DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)  
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)  
 DE MHC class II B locus 14 (Fragment).  
 OS Oreochromis niloticus (Nile tilapia) (Tilapia nilotica).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;  
 OC Acanthomorpha; Acanthopterygii; Percomorpha; Perciformes; Labroidei;  
 OC Cichlidae; Oreochromis.  
 OX NCBI\_TaxID=8128;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=98315113; PubMed=9649539;  
 RA Malaga-Trillo E., Zaleska-Rutczynska Z., McAndrew B., Vincek V.,  
 RA Figueroa F., Sultmann H., Klein J.;  
 RT "Linkage relationships and haplotype polymorphism among cichlid mhc  
 RT class II B loci."  
 RL Genetics 149:1527-1537(1998).  
 DR EMBL; AF050010; AAC41349.1; -.  
 FT NON\_TER 1 1  
 FT NON\_TER 11 11  
 SQ SEQUENCE 11 AA; 1349 MW; 81C12D8EB7341B41 CRC64;

Query Match 18.2%; Score 2; DB 7; Length 11;  
 Best Local Similarity 100.0%; Pred. No. 1.2e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 SR 5  
 ||  
 Db 8 SR 9

# RESULT 40

O77917

ID O77917 PRELIMINARY; PRT; 11 AA.  
AC O77917;  
DT 01-NOV-1998 (TrEMBLrel. 08, Created)  
DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)  
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)  
DE MHC class II B locus 14 (Fragment).  
OS Oreochromis niloticus (Nile tilapia) (Tilapia nilotica).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;  
OC Acanthomorpha; Acanthopterygii; Percomorpha; Perciformes; Labroidei;  
OC Cichlidae; Oreochromis.  
OX NCBI\_TaxID=8128;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=98315113; PubMed=9649539;  
RA Malaga-Trillo E., Zaleska-Rutczynska Z., McAndrew B., Vincek V.,  
RA Figueroa F., Sultmann H., Klein J.;  
RT "Linkage relationships and haplotype polymorphism among cichlid mhc  
RT class II B loci.";  
RL Genetics 149:1527-1537(1998).  
DR EMBL; AF050030; AAC41369.1; -.  
FT NON\_TER 1 1  
FT NON\_TER 11 11  
SQ SEQUENCE 11 AA; 1349 MW; 81C12D8EB7341B41 CRC64;

Query Match 18.2%; Score 2; DB 7; Length 11;  
Best Local Similarity 100.0%; Pred. No. 1.2e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 SR 5  
||  
Db 8 SR 9

# RESULT 41

O77902

ID O77902 PRELIMINARY; PRT; 11 AA.  
AC O77902;  
DT 01-NOV-1998 (TrEMBLrel. 08, Created)  
DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)  
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)  
DE MHC class II B locus 14 (Fragment).  
OS Oreochromis niloticus (Nile tilapia) (Tilapia nilotica).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;  
OC Acanthomorpha; Acanthopterygii; Percomorpha; Perciformes; Labroidei;  
OC Cichlidae; Oreochromis.  
OX NCBI\_TaxID=8128;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=98315113; PubMed=9649539;  
RA Malaga-Trillo E., Zaleska-Rutczynska Z., McAndrew B., Vincek V.,  
RA Figueroa F., Sultmann H., Klein J.;  
RT "Linkage relationships and haplotype polymorphism among cichlid mhc  
RT class II B loci.";

RL Genetics 149:1527-1537(1998).  
 DR EMBL; AF050012; AAC41351.1; -.  
 FT NON\_TER 1 1  
 FT NON\_TER 11 11  
 SQ SEQUENCE 11 AA; 1349 MW; 81C12D8EB7341B41 CRC64;

Query Match 18.2%; Score 2; DB 7; Length 11;  
 Best Local Similarity 100.0%; Pred. No. 1.2e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 SR 5  
 ||  
 Db 8 SR 9

# RESULT 42

O77921  
 ID O77921 PRELIMINARY; PRT; 11 AA.  
 AC O77921;  
 DT 01-NOV-1998 (TrEMBLrel. 08, Created)  
 DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)  
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)  
 DE MHC class II B locus 14 (Fragment).  
 OS Pseudotropheus sp. 'Pseudotropheus tropheops complex'.  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;  
 OC Acanthomorpha; Acanthopterygii; Percomorpha; Perciformes; Labroidei;  
 OC Cichlidae; Pseudotropheus.  
 OX NCBI\_TaxID=51796;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=98315113; PubMed=9649539;  
 RA Malaga-Trillo E., Zaleska-Rutczynska Z., McAndrew B., Vincek V.,  
 RA Figueroa F., Sultmann H., Klein J.;  
 RT "Linkage relationships and haplotype polymorphism among cichlid mhc  
 RT class II B loci.";  
 RL Genetics 149:1527-1537(1998).  
 DR EMBL; AF050034; AAC41373.1; -.  
 FT NON\_TER 1 1  
 FT NON\_TER 11 11  
 SQ SEQUENCE 11 AA; 1349 MW; 81C12D8EB7341B41 CRC64;

Query Match 18.2%; Score 2; DB 7; Length 11;  
 Best Local Similarity 100.0%; Pred. No. 1.2e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 SR 5  
 ||  
 Db 8 SR 9

# RESULT 43

O77901  
 ID O77901 PRELIMINARY; PRT; 11 AA.  
 AC O77901;  
 DT 01-NOV-1998 (TrEMBLrel. 08, Created)  
 DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)

DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)  
 DE MHC class II B locus 14 (Fragment).  
 OS Oreochromis niloticus (Nile tilapia) (Tilapia nilotica).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;  
 OC Acanthomorpha; Acanthopterygii; Percomorpha; Perciformes; Labroidei;  
 OC Cichlidae; Oreochromis.  
 OX NCBI\_TaxID=8128;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=98315113; PubMed=9649539;  
 RA Malaga-Trillo E., Zaleska-Rutczynska Z., McAndrew B., Vincek V.,  
 RA Figueroa F., Sultmann H., Klein J.;  
 RT "Linkage relationships and haplotype polymorphism among cichlid mhc  
 RT class II B loci.";  
 RL Genetics 149:1527-1537(1998).  
 DR EMBL; AF050011; AAC41350.1; -.  
 FT NON\_TER 1 1  
 FT NON\_TER 11 11  
 SQ SEQUENCE 11 AA; 1349 MW; 81C12D8EB7341B41 CRC64;  
  
 Query Match 18.2%; Score 2; DB 7; Length 11;  
 Best Local Similarity 100.0%; Pred. No. 1.2e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
 QY 4 SR 5  
 ||  
 Db 8 SR 9

RESULT 44

O77916  
 ID O77916 PRELIMINARY; PRT; 11 AA.  
 AC O77916;  
 DT 01-NOV-1998 (TrEMBLrel. 08, Created)  
 DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)  
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)  
 DE MHC class II B locus 14 (Fragment).  
 OS Oreochromis niloticus (Nile tilapia) (Tilapia nilotica).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;  
 OC Acanthomorpha; Acanthopterygii; Percomorpha; Perciformes; Labroidei;  
 OC Cichlidae; Oreochromis.  
 OX NCBI\_TaxID=8128;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=98315113; PubMed=9649539;  
 RA Malaga-Trillo E., Zaleska-Rutczynska Z., McAndrew B., Vincek V.,  
 RA Figueroa F., Sultmann H., Klein J.;  
 RT "Linkage relationships and haplotype polymorphism among cichlid mhc  
 RT class II B loci.";  
 RL Genetics 149:1527-1537(1998).  
 DR EMBL; AF050029; AAC41368.1; -.  
 FT NON\_TER 1 1  
 FT NON\_TER 11 11  
 SQ SEQUENCE 11 AA; 1349 MW; 81C12D8EB7341B41 CRC64;

Query Match 18.2%; Score 2; DB 7; Length 11;  
Best Local Similarity 100.0%; Pred. No. 1.2e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 SR 5  
||  
Db 8 SR 9

RESULT 45

O77905

ID O77905 PRELIMINARY; PRT; 11 AA.  
AC O77905;  
DT 01-NOV-1998 (TrEMBLrel. 08, Created)  
DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)  
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)  
DE MHC class II B locus 14 (Fragment).  
OS Oreochromis niloticus (Nile tilapia) (Tilapia nilotica).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;  
OC Acanthomorpha; Acanthopterygii; Percomorpha; Perciformes; Labroidei;  
OC Cichlidae; Oreochromis.  
OX NCBI\_TaxID=8128;  
RN [1]  
RP SEQUENCE FROM N.A..  
RX MEDLINE=98315113; PubMed=9649539;  
RA Malaga-Trillo E., Zaleska-Rutczynska Z., McAndrew B., Vincek V.,  
RA Figueroa F., Sultmann H., Klein J.;  
RT "Linkage relationships and haplotype polymorphism among cichlid mhc  
RT class II B loci."  
RL Genetics 149:1527-1537(1998).  
DR EMBL; AF050015; AAC41354.1; -.  
FT NON\_TER 1 1  
FT NON\_TER 11 11  
SQ SEQUENCE 11 AA; 1349 MW; 81C12D8EB7341B41 CRC64;

Query Match 18.2%; Score 2; DB 7; Length 11;  
Best Local Similarity 100.0%; Pred. No. 1.2e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 SR 5  
||  
Db 8 SR 9

RESULT 46

O77899

ID O77899 PRELIMINARY; PRT; 11 AA.  
AC O77899;  
DT 01-NOV-1998 (TrEMBLrel. 08, Created)  
DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)  
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)  
DE MHC class II B locus 14 (Fragment).  
OS Oreochromis niloticus (Nile tilapia) (Tilapia nilotica).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;  
OC Acanthomorpha; Acanthopterygii; Percomorpha; Perciformes; Labroidei;



OC Cichlidae; Oreochromis.  
 OX NCBI\_TaxID=8128;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=98315113; PubMed=9649539;  
 RA Malaga-Trillo E., Zaleska-Rutczynska Z., McAndrew B., Vincek V.,  
 RA Figueroa F., Sultmann H., Klein J.;  
 RT "Linkage relationships and haplotype polymorphism among cichlid mhc  
 RT class II B loci.";  
 RL Genetics 149:1527-1537(1998).  
 DR EMBL; AF050009; AAC41348.1; -.  
 FT NON\_TER 1 1  
 FT NON\_TER 11 11  
 SQ SEQUENCE 11 AA; 1349 MW; 81C12D8EB7341B41 CRC64;

Query Match 18.2%; Score 2; DB 7; Length 11;  
 Best Local Similarity 100.0%; Pred. No. 1.2e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 SR 5  
 ||  
 Db 8 SR 9

# RESULT 47

O78121  
 ID O78121 PRELIMINARY; PRT; 11 AA.  
 AC O78121;  
 DT 01-NOV-1998 (TrEMBLrel. 08, Created)  
 DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)  
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)  
 DE MHC class II B locus 12 (Fragment).  
 OS Oreochromis niloticus (Nile tilapia) (Tilapia nilotica).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;  
 OC Acanthomorpha; Acanthopterygii; Percomorpha; Perciformes; Labroidei;  
 OC Cichlidae; Oreochromis.  
 OX NCBI\_TaxID=8128;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=98315113; PubMed=9649539;  
 RA Malaga-Trillo E., Zaleska-Rutczynska Z., McAndrew B., Vincek V.,  
 RA Figueroa F., Sultmann H., Klein J.;  
 RT "Linkage relationships and haplotype polymorphism among cichlid mhc  
 RT class II B loci.";  
 RL Genetics 149:1527-1537(1998).  
 DR EMBL; AF050027; AAC41366.1; -.  
 FT NON\_TER 1 1  
 FT NON\_TER 11 11  
 SQ SEQUENCE 11 AA; 1362 MW; 03C12D8EB7341B54 CRC64;

Query Match 18.2%; Score 2; DB 7; Length 11;  
 Best Local Similarity 100.0%; Pred. No. 1.2e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 SR 5  
 ||

Db

8 SR 9

## RESULT 48

O77904

ID O77904 PRELIMINARY; PRT; 11 AA.  
 AC O77904;  
 DT 01-NOV-1998 (TrEMBLrel. 08, Created)  
 DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)  
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)  
 DE MHC class II B locus 14 (Fragment).  
 OS Oreochromis niloticus (Nile tilapia) (Tilapia nilotica).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;  
 OC Acanthomorpha; Acanthopterygii; Percomorpha; Perciformes; Labroidei;  
 OC Cichlidae; Oreochromis.  
 OX NCBI\_TaxID=8128;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=98315113; PubMed=9649539;  
 RA Malaga-Trillo E., Zaleska-Rutczynska Z., McAndrew B., Vincek V.,  
 RA Figueroa F., Sultmann H., Klein J.;  
 RT "Linkage relationships and haplotype polymorphism among cichlid mhc  
 RT class II B loci."  
 RL Genetics 149:1527-1537(1998).  
 DR EMBL; AF050014; AAC41353.1; -.  
 FT NON\_TER 1 1  
 FT NON\_TER 11 11  
 SQ SEQUENCE 11 AA; 1349 MW; 81C12D8EB7341B41 CRC64;

Query Match 18.2%; Score 2; DB 7; Length 11;  
 Best Local Similarity 100.0%; Pred. No. 1.2e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 SR 5

||

Db 8 SR 9

## RESULT 49

O77903

ID O77903 PRELIMINARY; PRT; 11 AA.  
 AC O77903;  
 DT 01-NOV-1998 (TrEMBLrel. 08, Created)  
 DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)  
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)  
 DE MHC class II B locus 14 (Fragment).  
 OS Oreochromis niloticus (Nile tilapia) (Tilapia nilotica).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;  
 OC Acanthomorpha; Acanthopterygii; Percomorpha; Perciformes; Labroidei;  
 OC Cichlidae; Oreochromis.  
 OX NCBI\_TaxID=8128;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=98315113; PubMed=9649539;  
 RA Malaga-Trillo E., Zaleska-Rutczynska Z., McAndrew B., Vincek V.,

RA Figueroa F., Sultmann H., Klein J.;  
 RT "Linkage relationships and haplotype polymorphism among cichlid mhc  
 RT class II B loci.";  
 RL Genetics 149:1527-1537(1998).  
 DR EMBL; AF050013; AAC41352.1; -.  
 FT NON\_TER 1 1  
 FT NON\_TER 11 11  
 SQ SEQUENCE 11 AA; 1349 MW; 81C12D8EB7341B41 CRC64;

Query Match 18.2%; Score 2; DB 7; Length 11;  
 Best Local Similarity 100.0%; Pred. No. 1.2e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 SR 5  
 ||  
 Db 8 SR 9

# RESULT 50

Q94V94

ID Q94V94 PRELIMINARY; PRT; 11 AA.  
 AC Q94V94;  
 DT 01-DEC-2001 (TrEMBLrel. 19, Created)  
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)  
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)  
 DE Cytochrome c oxidase subunit I (Fragment).  
 GN COI.  
 OS Varanus storri.  
 OG Mitochondrion.  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Lepidosauria; Squamata; Scleroglossa; Anguimorpha; Varanidae; Varanus.  
 OX NCBI\_TaxID=169855;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Ast J.C.;  
 RT "Mitochondrial DNA evidence and evolution in Varanoidea (Squamata).";  
 RL Cladistics 17:0-0(2001).  
 DR EMBL; AF407531; AAL10145.1; -.  
 DR GO; GO:0005739; C:mitochondrion; IEA.  
 KW Mitochondrion.  
 FT NON\_TER 11 11  
 SQ SEQUENCE 11 AA; 1387 MW; 8CBDEE80C7336411 CRC64;

Query Match 18.2%; Score 2; DB 8; Length 11;  
 Best Local Similarity 100.0%; Pred. No. 1.2e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 MT 8  
 ||  
 Db 1 MT 2

# RESULT 51

Q8ME62

ID Q8ME62 PRELIMINARY; PRT; 11 AA.  
 AC Q8ME62;  
 DT 01-OCT-2002 (TrEMBLrel. 22, Created)

DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)  
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)  
 DE Ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit  
 DE (Fragment).  
 GN RBCL.  
 OS Porphyra carolinensis.  
 OG Chloroplast.  
 OC Eukaryota; Rhodophyta; Bangiophyceae; Bangiales; Bangiaceae; Porphyra.  
 OX NCBI\_TaxID=76158;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=75;  
 RA Teasdale B.W., West A., Taylor H., Klein A.S.;  
 RT "A Simple Restriction Fragment Length Polymorphism (RFLP) Assay To  
 RT Discriminate Common Porphyra (Rhodophyta) Taxa From The Northwest  
 RT Atlantic.";  
 RL Submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases.  
 DR EMBL; AF414594; AAN03001.1; -.  
 DR GO; GO:0009507; C:chloroplast; IEA.  
 KW Chloroplast.  
 FT NON\_TER 1 1  
 SQ SEQUENCE 11 AA; 1177 MW; D8DE49C4B771AB02 CRC64;

Query Match 18.2%; Score 2; DB 8; Length 11;  
 Best Local Similarity 100.0%; Pred. No. 1.2e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 TA 9  
 ||  
 Db 8 TA 9

# RESULT 52

Q9G5W2

ID Q9G5W2 PRELIMINARY; PRT; 11 AA.  
 AC Q9G5W2;  
 DT 01-MAR-2001 (TrEMBLrel. 16, Created)  
 DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)  
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)  
 DE Cytochrome c oxidase subunit I (Fragment).  
 GN COI.  
 OS Laudakia tuberculata.  
 OG Mitochondrion.  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Lepidosauria; Squamata; Iguania; Acrodonta; Agamidae; Agaminae;  
 OC Laudakia.  
 OX NCBI\_TaxID=118215;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=22114082; PubMed=12118408;  
 RA Macey J.R., Schulte J.A. II, Larson A.;  
 RT "Evolution and information content of the mitochondrial genomic  
 RT structural features illustrated with acrodont lizards.";  
 RL Syst. Biol. 49:257-277(2000).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=22114081; PubMed=12118407;

RA Macey J.R., Schulte J.A. II, Larson A., Ananjeva N.B., Wang Y.,  
 RA Pethiyagoda R., Rastegar-Pouyani N., Papenfuss T.J.;  
 RT "Evaluating Trans-Tethys migration: An example using Acrodont lizard  
 RT phylogenetics.";  
 RL Syst. Biol. 49:233-256(2000).  
 DR EMBL; AF128514; AAG00779.1; -.  
 DR GO; GO:0005739; C:mitochondrion; IEA.  
 KW Mitochondrion.  
 FT NON\_TER 11 11  
 SQ SEQUENCE 11 AA; 1327 MW; A8F7371E336411A6 CRC64;

Query Match 18.2%; Score 2; DB 8; Length 11;  
 Best Local Similarity 100.0%; Pred. No. 1.2e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 MT 8  
 ||  
 Db 4 MT 5

# RESULT 53

Q9G622

ID Q9G622 PRELIMINARY; PRT; 11 AA.  
 AC Q9G622;  
 DT 01-MAR-2001 (TrEMBLrel. 16, Created)  
 DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)  
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)  
 DE Cytochrome c oxidase subunit I (Fragment).  
 GN COI.  
 OS Salea horsfieldii.  
 OG Mitochondrion.  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Lepidosauria; Squamata; Iguania; Acrodonta; Agamidae; Draconinae;  
 OC Salea.  
 OX NCBI\_TaxID=118233;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=22114082; PubMed=12118408;  
 RA Macey J.R., Schulte J.A. II, Larson A.;  
 RT "Evolution and information content of the mitochondrial genomic  
 RT structural features illustrated with acrodont lizards.";  
 RL Syst. Biol. 49:257-277(2000).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=22114081; PubMed=12118407;  
 RA Macey J.R., Schulte J.A. II, Larson A., Ananjeva N.B., Wang Y.,  
 RA Pethiyagoda R., Rastegar-Pouyani N., Papenfuss T.J.;  
 RT "Evaluating Trans-Tethys migration: An example using Acrodont lizard  
 RT phylogenetics.";  
 RL Syst. Biol. 49:233-256(2000).  
 DR EMBL; AF128490; AAG00707.1; -.  
 DR GO; GO:0005739; C:mitochondrion; IEA.  
 KW Mitochondrion.  
 FT NON\_TER 11 11  
 SQ SEQUENCE 11 AA; 1264 MW; 5B2C371E33640DD7 CRC64;

Query Match 18.2%; Score 2; DB 8; Length 11;

Best Local Similarity 100.0%; Pred. No. 1.2e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AR 2  
||  
Db 5 AR 6

RESULT 54

Q94VG8

ID Q94VG8 PRELIMINARY; PRT; 11 AA.  
AC Q94VG8;  
DT 01-DEC-2001 (TrEMBLrel. 19, Created)  
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)  
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)  
DE Cytochrome c oxidase subunit I (Fragment).  
GN COI.  
OS Varanus gouldii (Gould's monitor).  
OG Mitochondrion.  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Lepidosauria; Squamata; Scleroglossa; Anguimorpha; Varanidae; Varanus.  
OX NCBI\_TaxID=62042;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Ast J.C.;  
RT "Mitochondrial DNA evidence and evolution in Varanoidea (Squamata).";  
RL Cladistics 17:0-0(2001).  
DR EMBL; AF407502; AAL10060.1; -.  
DR GO; GO:0005739; C:mitochondrion; IEA.  
KW Mitochondrion.  
FT NON\_TER 11 11  
SQ SEQUENCE 11 AA; 1370 MW; 8E6DEE80C7336411 CRC64;

Query Match 18.2%; Score 2; DB 8; Length 11;  
Best Local Similarity 100.0%; Pred. No. 1.2e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 MT 8  
||  
Db 1 MT 2

RESULT 55

Q9G5Y6

ID Q9G5Y6 PRELIMINARY; PRT; 11 AA.  
AC Q9G5Y6;  
DT 01-MAR-2001 (TrEMBLrel. 16, Created)  
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)  
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
DE Cytochrome c oxidase subunit I (Fragment).  
GN COI.  
OS Agama agama (Red-headed rock agama).  
OG Mitochondrion.  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Lepidosauria; Squamata; Iguania; Acrodonta; Agamidae; Agaminae; Agama.  
OX NCBI\_TaxID=103336;  
RN [1]

RP SEQUENCE FROM N.A.  
 RX MEDLINE=22114082; PubMed=12118408;  
 RA Macey J.R., Schulte J.A. II, Larson A.;  
 RT "Evolution and information content of the mitochondrial genomic  
 RT structural features illustrated with acrodont lizards.";  
 RL Syst. Biol. 49:257-277(2000).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=22114081; PubMed=12118407;  
 RA Macey J.R., Schulte J.A. II, Larson A., Ananjeva N.B., Wang Y.,  
 RA Pethiyagoda R., Rastegar-Pouyani N., Papenfuss T.J.;  
 RT "Evaluating Trans-Tethys migration: An example using Acrodont lizard  
 RT phylogenetics.";  
 RL Syst. Biol. 49:233-256(2000).  
 DR EMBL; AF128504; AAG00749.1; -.  
 DR GO; GO:0005739; C:mitochondrion; IEA.  
 KW Mitochondrion.  
 FT NON\_TER 11 11  
 SQ SEQUENCE 11 AA; 1324 MW; 9D52EC1E336415A1 CRC64;

Query Match 18.2%; Score 2; DB 8; Length 11;  
 Best Local Similarity 100.0%; Pred. No. 1.2e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 MT 8  
 ||  
 Db 1 MT 2

# RESULT 56

Q8MEL7

ID Q8MEL7 PRELIMINARY; PRT; 11 AA.  
 AC Q8MEL7;  
 DT 01-OCT-2002 (TrEMBLrel. 22, Created)  
 DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)  
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)  
 DE Ribosomal protein 16 (Fragment).  
 GN RPL16.  
 OS Sida hookeriana.  
 OG Chloroplast.  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;  
 OC eurosids II; Malvales; Malvaceae; Malvoideae; Sida.  
 OX NCBI\_TaxID=108446;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Pfeil B.E., Brubaker C.L., Craven L.A., Crisp M.D.;  
 RT "Phylogeny of Hibiscus and the tribe Hibisceae (Malvaceae) using  
 RT chloroplast DNA sequences of ndhF and the rpl16 intron.";  
 RL Syst. Bot. 27:333-350(2002).  
 DR EMBL; AF384624; AAM50396.1; -.  
 DR GO; GO:0009507; C:chloroplast; IEA.  
 KW Chloroplast.  
 FT NON\_TER 1 1  
 FT NON\_TER 11 11  
 SQ SEQUENCE 11 AA; 1470 MW; 7227C351D32409D4 CRC64;

Query Match 18.2%; Score 2; DB 8; Length 11;  
Best Local Similarity 100.0%; Pred. No. 1.2e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 RK 3  
||  
Db 6 RK 7

RESULT 57

Q9G5Y0

ID Q9G5Y0 PRELIMINARY; PRT; 11 AA.  
AC Q9G5Y0;  
DT 01-MAR-2001 (TrEMBLrel. 16, Created)  
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)  
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)  
DE Cytochrome c oxidase subunit I (Fragment).  
GN COI.  
OS Pseudotrapelus sinaitus.  
OG Mitochondrion.  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Lepidosauria; Squamata; Iguania; Acrodonta; Agamidae; Agaminae;  
OC Pseudotrapelus.  
OX NCBI\_TaxID=118229;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=22114082; PubMed=12118408;  
RA Macey J.R., Schulte J.A. II, Larson A.;  
RT "Evolution and information content of the mitochondrial genomic  
RT structural features illustrated with acrodont lizards."  
RL Syst. Biol. 49:257-277(2000).  
RN [2]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=22114081; PubMed=12118407;  
RA Macey J.R., Schulte J.A. II, Larson A., Ananjeva N.B., Wang Y.,  
RA Pethiyagoda R., Rastegar-Pouyani N., Papenfuss T.J.;  
RT "Evaluating Trans-Tethys migration: An example using Acrodont lizard  
RT phylogenetics."  
RL Syst. Biol. 49:233-256(2000).  
DR EMBL; AF128507; AAG00758.1; -.  
DR GO; GO:0005739; C:mitochondrion; IEA.  
KW Mitochondrion.  
FT NON\_TER 11 11  
SQ SEQUENCE 11 AA; 1374 MW; B05439FE336415B6 CRC64;

Query Match 18.2%; Score 2; DB 8; Length 11;  
Best Local Similarity 100.0%; Pred. No. 1.2e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 SR 5  
||  
Db 5 SR 6

RESULT 58

Q9G5W5

ID Q9G5W5 PRELIMINARY; PRT; 11 AA.



AC Q9G5W5;  
 DT 01-MAR-2001 (TrEMBLrel. 16, Created)  
 DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)  
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)  
 DE Cytochrome c oxidase subunit I (Fragment).  
 GN COI.  
 OS Laudakia nupta.  
 OG Mitochondrion.  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Lepidosauria; Squamata; Iguania; Acrodonta; Agamidae; Agaminae;  
 OC Laudakia.  
 OX NCBI\_TaxID=118212;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=22114082; PubMed=12118408;  
 RA Macey J.R., Schulte J.A. II, Larson A.;  
 RT "Evolution and information content of the mitochondrial genomic  
 RT structural features illustrated with acrodont lizards.";  
 RL Syst. Biol. 49:257-277(2000).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=22114081; PubMed=12118407;  
 RA Macey J.R., Schulte J.A. II, Larson A., Ananjeva N.B., Wang Y.,  
 RA Pethiyagoda R., Rastegar-Pouyani N., Papenfuss T.J.;  
 RT "Evaluating Trans-Tethys migration: An example using Acrodont lizard  
 RT phylogenetics.";  
 RL Syst. Biol. 49:233-256(2000).  
 DR EMBL; AF128513; AAG00776.1; -.  
 DR GO; GO:0005739; C:mitochondrion; IEA.  
 KW Mitochondrion.  
 FT NON\_TER 11 11  
 SQ SEQUENCE 11 AA; 1361 MW; A8F73710D36411A6 CRC64;

Query Match 18.2%; Score 2; DB 8; Length 11;  
 Best Local Similarity 100.0%; Pred. No. 1.2e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 MT 8  
 ||  
 Db 4 MT 5

# RESULT 59

Q9G607

ID Q9G607 PRELIMINARY; PRT; 11 AA.

AC Q9G607;

DT 01-MAR-2001 (TrEMBLrel. 16, Created)

DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)

DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)

DE Cytochrome c oxidase subunit I (Fragment).

GN COI.

OS Aphaniotis fusca.

OG Mitochondrion.

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Lepidosauria; Squamata; Iguania; Acrodonta; Agamidae; Draconinae;

OC Aphaniotis.

OX NCBI\_TaxID=89036;

RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=22114082; PubMed=12118408;  
 RA Macey J.R., Schulte J.A. II, Larson A.;  
 RT "Evolution and information content of the mitochondrial genomic  
 RT structural features illustrated with acrodont lizards.";  
 RL Syst. Biol. 49:257-277(2000).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=22114081; PubMed=12118407;  
 RA Macey J.R., Schulte J.A. II, Larson A., Ananjeva N.B., Wang Y.,  
 RA Pethiyagoda R., Rastegar-Pouyani N., Papenfuss T.J.;  
 RT "Evaluating Trans-Tethys migration: An example using Acrodont lizard  
 RT phylogenetics.";  
 RL Syst. Biol. 49:233-256(2000).  
 DR EMBL; AF128495; AAG00722.1; -.  
 DR GO; GO:0005739; C:mitochondrion; IEA.  
 KW Mitochondrion.  
 FT NON\_TER 11 11  
 SQ SEQUENCE 11 AA; 1389 MW; A68E371E336411A6 CRC64;

Query Match 18.2%; Score 2; DB 8; Length 11;  
 Best Local Similarity 100.0%; Pred. No. 1.2e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 MT 8  
 ||  
 Db 4 MT 5

# RESULT 60

Q94V77

ID Q94V77 PRELIMINARY; PRT; 11 AA.  
 AC Q94V77;  
 DT 01-DEC-2001 (TrEMBLrel. 19, Created)  
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)  
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)  
 DE Cytochrome c oxidase subunit I (Fragment).  
 GN COI.  
 OS Heloderma suspectum (Gila monster).  
 OG Mitochondrion.  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Lepidosauria; Squamata; Scleroglossa; Anguimorpha; Helodermatidae;  
 OC Heloderma.  
 OX NCBI\_TaxID=8554;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Ast J.C.;  
 RT "Mitochondrial DNA evidence and evolution in Varanoidea (Squamata).";  
 RL Cladistics 17:0-0(2001).  
 DR EMBL; AF407540; AAL10172.1; -.  
 DR GO; GO:0005739; C:mitochondrion; IEA.  
 KW Mitochondrion.  
 FT NON\_TER 11 11  
 SQ SEQUENCE 11 AA; 1396 MW; 8E3A6DE0D5A36411 CRC64;

Query Match 18.2%; Score 2; DB 8; Length 11;

Best Local Similarity 100.0%; Pred. No. 1.2e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 MT 8  
||  
Db 1 MT 2

RESULT 61

O79985

ID O79985 PRELIMINARY; PRT; 11 AA.  
AC O79985;  
DT 01-NOV-1998 (TrEMBLrel. 08, Created)  
DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)  
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)  
DE Cytochrome C oxidase subunit I (Fragment).  
GN COI.  
OS Laudakia caucasia.  
OG Mitochondrion.  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Lepidosauria; Squamata; Iguania; Acrodonta; Agamidae; Agaminae;  
OC Laudakia.  
OX NCBI\_TaxID=71145;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=98424476; PubMed=9751922;  
RA Macey J.R., Schulte J.A. II, Ananjeva N.B., Larson A.,  
RA Rastegar-Pouyani N., Shammakov S.M., Papenfuss T.J.;  
RT "Phylogenetic relationships among Agamid lizards of the Laudakia  
RT caucasia species group: testing hypotheses of biogeographic  
RT fragmentation and an area cladogram for the Iranian Plateau.";  
RL Mol. Phylogenet. Evol. 10:118-131(1998).  
RN [2]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=20179532; PubMed=10712852;  
RA Macey J.R., Schulte J.A. II, Kami H.G., Ananjeva N.B., Larson A.,  
RA Papenfuss T.J.;  
RT "Testing hypotheses of vicariance in the agamid lizard laudakia  
RT caucasia from mountain ranges on the northern iranian plateau.";  
RL Mol. Phylogenet. Evol. 14:479-483(2000).  
DR EMBL; AF028687; AAC99614.1; -.  
DR EMBL; AF028681; AAC99596.1; -.  
DR EMBL; AF028682; AAC99599.1; -.  
DR EMBL; AF028683; AAC99602.1; -.  
DR EMBL; AF028684; AAC99605.1; -.  
DR EMBL; AF028685; AAC99608.1; -.  
DR EMBL; AF028686; AAC99611.1; -.  
DR EMBL; AF172705; AAF65208.1; -.  
DR EMBL; AF172704; AAF65205.1; -.  
DR PIR; T12264; T12264.  
DR GO; GO:0005739; C:mitochondrion; IEA.  
KW Mitochondrion.  
FT NON\_TER 11 11  
SQ SEQUENCE 11 AA; 1361 MW; A8F73710D36411A6 CRC64;

Query Match 18.2%; Score 2; DB 8; Length 11;  
Best Local Similarity 100.0%; Pred. No. 1.2e+05;

Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 MT 8  
||  
Db 4 MT 5

RESULT 62

Q9G359

ID Q9G359 PRELIMINARY; PRT; 11 AA.  
AC Q9G359;  
DT 01-MAR-2001 (TrEMBLrel. 16, Created)  
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)  
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)  
DE Cytochrome c oxidase subunit I (Fragment).  
GN COI.  
OS Japalura flaviceps.  
OG Mitochondrion.  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Lepidosauria; Squamata; Iguania; Acrodonta; Agamidae; Draconinae;  
OC Japalura.  
OX NCBI\_TaxID=52218;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=97153820; PubMed=9000751;  
RA Macey J.R., Larson A., Ananjeva N.B., Papenfuss T.J.;  
RT "Replication slippage may cause parallel evolution in the secondary  
RT structures of mitochondrial transfer RNAs.";  
RL Mol. Biol. Evol. 14:30-39(1997).  
RN [2]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=22114082; PubMed=12118408;  
RA Macey J.R., Schulte J.A. II, Larson A.;  
RT "Evolution and information content of the mitochondrial genomic  
RT structural features illustrated with acrodont lizards.";  
RL Syst. Biol. 49:257-277(2000).  
RN [3]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=22114081; PubMed=12118407;  
RA Macey J.R., Schulte J.A. II, Larson A., Ananjeva N.B., Wang Y.,  
RA Pethiyagoda R., Rastegar-Pouyani N., Papenfuss T.J.;  
RT "Evaluating Trans-Tethys migration: An example using Acrodont lizard  
RT phylogenetics.";  
RL Syst. Biol. 49:233-256(2000).  
DR EMBL; AF128500; AAG00737.1; -.  
DR GO; GO:0005739; C:mitochondrion; IEA.  
KW Mitochondrion.  
FT NON TER 11 11  
SQ SEQUENCE 11 AA; 1341 MW; 538E371E33640DD7 CRC64;

Query Match 18.2%; Score 2; DB 8; Length 11;

Best Local Similarity 100.0%; Pred. No. 1.2e+05;

Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AR 2  
||  
Db 5 AR 6

RESULT 63

Q8MEM2

ID Q8MEM2 PRELIMINARY; PRT; 11 AA.  
 AC Q8MEM2;  
 DT 01-OCT-2002 (TrEMBLrel. 22, Created)  
 DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)  
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)  
 DE Ribosomal protein 16 (Fragment).  
 GN RPL16.  
 OS Lagunaria patersonia.  
 OG Chloroplast.  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;  
 OC eurosids II; Malvales; Malvaceae; Malvoideae; Lagunaria.  
 OX NCBI\_TaxID=183274;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Pfeil B.E., Brubaker C.L., Craven L.A., Crisp M.D.;  
 RT "Phylogeny of Hibiscus and the tribe Hibisceae (Malvaceae) using  
 RT chloroplast DNA sequences of ndhF and the rpl16 intron.";  
 RL Syst. Bot. 27:333-350(2002).  
 DR EMBL; AF384616; AAM50388.1; -.  
 DR GO; GO:0009507; C:chloroplast; IEA.  
 KW Chloroplast.  
 FT NON\_TER 1 1  
 FT NON\_TER 11 11  
 SQ SEQUENCE 11 AA; 1470 MW; 7227C351D32409D4 CRC64;

Query Match 18.2%; Score 2; DB 8; Length 11;  
 Best Local Similarity 100.0%; Pred. No. 1.2e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 RK 3  
 ||  
 Db 6 RK 7

RESULT 64

Q9G649

ID Q9G649 PRELIMINARY; PRT; 11 AA.  
 AC Q9G649;  
 DT 01-MAR-2001 (TrEMBLrel. 16, Created)  
 DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)  
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)  
 DE Cytochrome c oxidase subunit I (Fragment).  
 GN COI.  
 OS Otocryptis wiegmanni.  
 OG Mitochondrion.  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Lepidosauria; Squamata; Iguania; Acrodonta; Agamidae; Draconinae;  
 OC Otocryptis.  
 OX NCBI\_TaxID=118220;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=22114082; PubMed=12118408;

RA Macey J.R., Schulte J.A. II, Larson A.;  
 RT "Evolution and information content of the mitochondrial genomic  
 RT structural features illustrated with acrodont lizards.";  
 RL Syst. Biol. 49:257-277(2000).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=22114081; PubMed=12118407;  
 RA Macey J.R., Schulte J.A. II, Larson A., Ananjeva N.B., Wang Y.,  
 RA Pethiyagoda R., Rastegar-Pouyani N., Papenfuss T.J.;  
 RT "Evaluating Trans-Tethys migration: An example using Acrodont lizard  
 RT phylogenetics.";  
 RL Syst. Biol. 49:233-256(2000).  
 DR EMBL; AF128480; AAG00677.1; -.  
 DR GO; GO:0005739; C:mitochondrion; IEA.  
 KW Mitochondrion.  
 FT NON\_TER 11 11  
 SQ SEQUENCE 11 AA; 1347 MW; 932D3710D3640DC1 CRC64;

Query Match 18.2%; Score 2; DB 8; Length 11;  
 Best Local Similarity 100.0%; Pred. No. 1.2e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AR 2  
 ||  
 Db 5 AR 6

# RESULT 65

Q9G643

ID Q9G643 PRELIMINARY; PRT; 11 AA.  
 AC Q9G643;  
 DT 01-MAR-2001 (TrEMBLrel. 16, Created)  
 DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)  
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)  
 DE Cytochrome c oxidase subunit I (Fragment).  
 GN COI.  
 OS Calotes calotes.  
 OG Mitochondrion.  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Lepidosauria; Squamata; Iguania; Acrodonta; Agamidae; Draconinae;  
 OC Calotes.  
 OX NCBI\_TaxID=118093;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=22114082; PubMed=12118408;  
 RA Macey J.R., Schulte J.A. II, Larson A.;  
 RT "Evolution and information content of the mitochondrial genomic  
 RT structural features illustrated with acrodont lizards.";  
 RL Syst. Biol. 49:257-277(2000).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=22114081; PubMed=12118407;  
 RA Macey J.R., Schulte J.A. II, Larson A., Ananjeva N.B., Wang Y.,  
 RA Pethiyagoda R., Rastegar-Pouyani N., Papenfuss T.J.;  
 RT "Evaluating Trans-Tethys migration: An example using Acrodont lizard  
 RT phylogenetics.";  
 RL Syst. Biol. 49:233-256(2000).

DR EMBL; AF128482; AAG00683.1; -.  
DR GO; GO:0005739; C:mitochondrion; IEA.  
KW Mitochondrion.  
FT NON\_TER 11 11  
SQ SEQUENCE 11 AA; 1373 MW; BE2D371E336411A6 CRC64;

Query Match 18.2%; Score 2; DB 8; Length 11;  
Best Local Similarity 100.0%; Pred. No. 1.2e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 MT 8  
||  
Db 4 MT 5

#### RESULT 66

##### Q9G5X4

ID Q9G5X4 PRELIMINARY; PRT; 11 AA.  
AC Q9G5X4;  
DT 01-MAR-2001 (TrEMBLrel. 16, Created)  
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)  
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)  
DE Cytochrome c oxidase subunit I (Fragment).  
GN COI.  
OS Trapelus agilis.  
OG Mitochondrion.  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Lepidosauria; Squamata; Iguania; Acrodonta; Agamidae; Agaminae;  
OC Trapelus.  
OX NCBI\_TaxID=52210;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=22114082; PubMed=12118408;  
RA Macey J.R., Schulte J.A. II, Larson A.;  
RT "Evolution and information content of the mitochondrial genomic  
RT structural features illustrated with acrodont lizards.";  
RL Syst. Biol. 49:257-277(2000).  
RN [2]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=22114081; PubMed=12118407;  
RA Macey J.R., Schulte J.A. II, Larson A., Ananjeva N.B., Wang Y.,  
RA Pethiyagoda R., Rastegar-Pouyani N., Papenfuss T.J.;  
RT "Evaluating Trans-Tethys migration: An example using Acrodont lizard  
RT phylogenetics.";  
RL Syst. Biol. 49:233-256(2000).  
DR EMBL; AF128509; AAG00764.1; -.  
DR GO; GO:0005739; C:mitochondrion; IEA.  
KW Mitochondrion.  
FT NON\_TER 11 11  
SQ SEQUENCE 11 AA; 1391 MW; BFC73710D36411A6 CRC64;

Query Match 18.2%; Score 2; DB 8; Length 11;  
Best Local Similarity 100.0%; Pred. No. 1.2e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 MT 8  
||

Db

4 MT 5

RESULT 67

Q94V74

ID Q94V74 PRELIMINARY; PRT; 11 AA.  
AC Q94V74;  
DT 01-DEC-2001 (TrEMBLrel. 19, Created)  
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)  
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)  
DE Cytochrome c oxidase subunit I (Fragment).  
GN COI.  
OS Lanthanotus borneensis.  
OG Mitochondrion.  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Lepidosauria; Squamata; Scleroglossa; Anguimorpha; Lanthanotidae;  
OC Lanthanotus.  
OX NCBI\_TaxID=62058;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Ast J.C.;  
RT "Mitochondrial DNA evidence and evolution in Varanoidea (Squamata).";  
RL Cladistics 17:0-0(2001).  
DR EMBL; AF407541; AAL10175.1; -.  
DR GO; GO:0005739; C:mitochondrion; IEA.  
KW Mitochondrion.  
FT NON\_TER 11 11  
SQ SEQUENCE 11 AA; 1388 MW; 8F28EE80C7336411 CRC64;

Query Match 18.2%; Score 2; DB 8; Length 11;  
Best Local Similarity 100.0%; Pred. No. 1.2e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 MT 8  
||  
Db 1 MT 2

RESULT 68

Q8MES5

ID Q8MES5 PRELIMINARY; PRT; 11 AA.  
AC Q8MES5;  
DT 01-OCT-2002 (TrEMBLrel. 22, Created)  
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)  
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)  
DE Ribosomal protein 16 (Fragment).  
GN RPL16.  
OS Abelmoschus manihot.  
OG Chloroplast.  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;  
OC eurosids II; Malvales; Malvaceae; Malvoideae; Abelmoschus.  
OX NCBI\_TaxID=183220;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Pfeil B.E., Brubaker C.L., Craven L.A., Crisp M.D.;  
RT "Phylogeny of Hibiscus and the tribe Hibisceae (Malvaceae) using



RT chloroplast DNA sequences of ndhF and the rpl16 intron.";  
 RL Syst. Bot. 27:333-350(2002).  
 DR EMBL; AF384561; AAM50399.1; -.  
 DR GO; GO:0009507; C:chloroplast; IEA.  
 KW Chloroplast.  
 FT NON\_TER 1 1  
 FT NON\_TER 11 11  
 SQ SEQUENCE 11 AA; 1470 MW; 7227C351D32409D4 CRC64;

Query Match 18.2%; Score 2; DB 8; Length 11;  
 Best Local Similarity 100.0%; Pred. No. 1.2e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 RK 3  
 ||  
 Db 6 RK 7

# RESULT 69

Q9GD68

ID Q9GD68 PRELIMINARY; PRT; 11 AA.  
 AC Q9GD68;  
 DT 01-MAR-2001 (TrEMBLrel. 16, Created)  
 DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)  
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)  
 DE Ribosomal protein S16 (Fragment).  
 GN RPS16.  
 OS Elaeis guineensis var. tenera (Oil palm).  
 OG Chloroplast.  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; Liliopsida; Arecaceae; Arecoideae;  
 OC Cocoeae; Elaeidinae; Elaeis.  
 OX NCBI\_TaxID=51953;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Leaf;  
 RA Asmussen C.B., Chase M.W.;  
 RT "Coding and noncoding plastid DNA in palm systematics.";  
 RL Submitted (JUL-2000) to the EMBL/GenBank/DDBJ databases.  
 DR EMBL; AJ404952; CAC17867.1; -.  
 DR GO; GO:0009507; C:chloroplast; IEA.  
 KW Chloroplast.  
 FT NON\_TER 1 1  
 FT NON\_TER 11 11  
 SQ SEQUENCE 11 AA; 1386 MW; 634693A666C2C044 CRC64;

Query Match 18.2%; Score 2; DB 8; Length 11;  
 Best Local Similarity 100.0%; Pred. No. 1.2e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 AI 10  
 ||  
 Db 1 AI 2

# RESULT 70

Q9G350

ID Q9G350 PRELIMINARY; PRT; 11 AA.  
 AC Q9G350;  
 DT 01-MAR-2001 (TrEMBLrel. 16, Created)  
 DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)  
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)  
 DE Cytochrome c oxidase subunit I (Fragment).  
 GN COI.  
 OS Laudakia sacra.  
 OG Mitochondrion.  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Lepidosauria; Squamata; Iguania; Acrodonta; Agamidae; Agaminae;  
 OC Laudakia.  
 OX NCBI\_TaxID=52204;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=97153820; PubMed=9000751;  
 RA Macey J.R., Larson A., Ananjeva N.B., Papenfuss T.J.;  
 RT "Replication slippage may cause parallel evolution in the secondary  
 RT structures of mitochondrial transfer RNAs.";  
 RL Mol. Biol. Evol. 14:30-39(1997).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=22114082; PubMed=12118408;  
 RA Macey J.R., Schulte J.A. II, Larson A.;  
 RT "Evolution and information content of the mitochondrial genomic  
 RT structural features illustrated with acrodont lizards.";  
 RL Syst. Biol. 49:257-277(2000).  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=22114081; PubMed=12118407;  
 RA Macey J.R., Schulte J.A. II, Larson A., Ananjeva N.B., Wang Y.,  
 RA Pethiyagoda R., Rastegar-Pouyani N., Papenfuss T.J.;  
 RT "Evaluating Trans-Tethys migration: An example using Acrodont lizard  
 RT phylogenetics.";  
 RL Syst. Biol. 49:233-256(2000).  
 DR EMBL; AF128515; AAG00782.1; -.  
 DR GO; GO:0005739; C:mitochondrion; IEA.  
 KW Mitochondrion.  
 FT NON\_TER 11 11  
 SQ SEQUENCE 11 AA; 1361 MW; A8F73710D36411A6 CRC64;  
  
 Query Match 18.2%; Score 2; DB 8; Length 11;  
 Best Local Similarity 100.0%; Pred. No. 1.2e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
 Qy 7 MT 8  
 ||  
 Db 4 MT 5

RESULT 71

Q8WD17

ID Q8WD17 PRELIMINARY; PRT; 11 AA.  
 AC Q8WD17;  
 DT 01-MAR-2002 (TrEMBLrel. 20, Created)  
 DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)  
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)

DE Cytochrome c oxidase subunit I (Fragment).  
GN COI.  
OS Ctenophorus reticulatus (Western netted dragon).  
OG Mitochondrion.  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Lepidosauria; Squamata; Iguania; Acrodonta; Agamidae; Amphibolurinae;  
OC Ctenophorus.  
OX NCBI\_TaxID=180002;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Melville J., Schulte J.A. II, Larson A.;  
RT "A molecular phylogenetic study of ecological diversification in the  
RT Australian lizard genus Ctenophorus."  
RL Submitted (MAY-2001) to the EMBL/GenBank/DDBJ databases.  
DR EMBL; AF375634; AAL40433.1; -.  
DR GO; GO:0005739; C:mitochondrion; IEA.  
KW Mitochondrion.  
FT NON\_TER 11 11  
SQ SEQUENCE 11 AA; 1313 MW; A8F7371E336415B6 CRC64;

Query Match 18.2%; Score 2; DB 8; Length 11;  
Best Local Similarity 100.0%; Pred. No. 1.2e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 SR 5  
||  
Db 5 SR 6

# RESULT 72

Q9G5Z8

ID Q9G5Z8 PRELIMINARY; PRT; 11 AA.  
AC Q9G5Z8;  
DT 01-MAR-2001 (TrEMBLrel. 16, Created)  
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)  
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)  
DE Cytochrome c oxidase subunit I (Fragment).  
GN COI.  
OS Acanthosaura lepidogaster.  
OG Mitochondrion.  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Lepidosauria; Squamata; Iguania; Acrodonta; Agamidae; Draconinae;  
OC Acanthosaura.  
OX NCBI\_TaxID=118088;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=22114082; PubMed=12118408;  
RA Macey J.R., Schulte J.A. II, Larson A.;  
RT "Evolution and information content of the mitochondrial genomic  
RT structural features illustrated with acrodont lizards."  
RL Syst. Biol. 49:257-277(2000).  
RN [2]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=22114081; PubMed=12118407;  
RA Macey J.R., Schulte J.A. II, Larson A., Ananjeva N.B., Wang Y.,  
RA Pethiyagoda R., Rastegar-Pouyani N., Papenfuss T.J.;  
RT "Evaluating Trans-Tethys migration: An example using Acrodont lizard

RT phylogenetics.";  
 RL Syst. Biol. 49:233-256(2000).  
 DR EMBL; AF128499; AAG00734.1; -.  
 DR GO; GO:0005739; C:mitochondrion; IEA.  
 KW Mitochondrion.  
 FT NON\_TER 11 11  
 SQ SEQUENCE 11 AA; 1279 MW; 5DF7371E33640DD7 CRC64;

Query Match 18.2%; Score 2; DB 8; Length 11;  
 Best Local Similarity 100.0%; Pred. No. 1.2e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AR 2  
 ||  
 Db 5 AR 6

# RESULT 73

Q9G368

ID Q9G368 PRELIMINARY; PRT; 11 AA.  
 AC Q9G368;  
 DT 01-MAR-2001 (TrEMBLrel. 16, Created)  
 DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)  
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)  
 DE Cytochrome c oxidase subunit I (Fragment).  
 GN COI.  
 OS Draco blanfordii.  
 OG Mitochondrion.  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Lepidosauria; Squamata; Iguania; Acrodonta; Agamidae; Draconinae;  
 OC Draco.  
 OX NCBI\_TaxID=89021;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=97153820; PubMed=9000751;  
 RA Macey J.R., Larson A., Ananjeva N.B., Papenfuss T.J.;  
 RT "Replication slippage may cause parallel evolution in the secondary  
 RT structures of mitochondrial transfer RNAs.";  
 RL Mol. Biol. Evol. 14:30-39(1997).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=22114082; PubMed=12118408;  
 RA Macey J.R., Schulte J.A. II, Larson A.;  
 RT "Evolution and information content of the mitochondrial genomic  
 RT structural features illustrated with acrodont lizards.";  
 RL Syst. Biol. 49:257-277(2000).  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=22114081; PubMed=12118407;  
 RA Macey J.R., Schulte J.A. II, Larson A., Ananjeva N.B., Wang Y.,  
 RA Pethiyagoda R., Rastegar-Pouyani N., Papenfuss T.J.;  
 RT "Evaluating Trans-Tethys migration: An example using Acrodont lizard  
 RT phylogenetics.";  
 RL Syst. Biol. 49:233-256(2000).  
 DR EMBL; AF128477; AAG00668.1; -.  
 DR GO; GO:0005739; C:mitochondrion; IEA.  
 KW Mitochondrion.

FT NON\_TER 11 11  
SQ SEQUENCE 11 AA; 1341 MW; 4B2D371E336415B7 CRC64;

Query Match 18.2%; Score 2; DB 8; Length 11;  
Best Local Similarity 100.0%; Pred. No. 1.2e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 SR 5  
||  
Db 5 SR 6

RESULT 74

Q9G5W8

ID Q9G5W8 PRELIMINARY; PRT; 11 AA.

AC Q9G5W8;

DT 01-MAR-2001 (TrEMBLrel. 16, Created)

DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)

DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)

DE Cytochrome c oxidase subunit I (Fragment).

GN COI.

OS Trapelus savignyi.

OG Mitochondrion.

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Lepidosauria; Squamata; Iguania; Acrodonta; Agamidae; Agaminae;

OC Trapelus.

OX NCBI\_TaxID=118240;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=22114082; PubMed=12118408;

RA Macey J.R., Schulte J.A. II, Larson A.;

RT "Evolution and information content of the mitochondrial genomic

RT structural features illustrated with acrodont lizards.";

RL Syst. Biol. 49:257-277(2000).

RN [2]

RP SEQUENCE FROM N.A.

RX MEDLINE=22114081; PubMed=12118407;

RA Macey J.R., Schulte J.A. II, Larson A., Ananjeva N.B., Wang Y.,

RA Pethiyagoda R., Rastegar-Pouyani N., Papenfuss T.J.;

RT "Evaluating Trans-Tethys migration: An example using Acrodont lizard

RT phylogenetics.";

RL Syst. Biol. 49:233-256(2000).

DR EMBL; AF128512; AAG00773.1; -.

DR GO; GO:0005739; C:mitochondrion; IEA.

KW Mitochondrion.

FT NON\_TER 11 11

SQ SEQUENCE 11 AA; 1361 MW; A8F73710D36411A6 CRC64;

Query Match 18.2%; Score 2; DB 8; Length 11;  
Best Local Similarity 100.0%; Pred. No. 1.2e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 MT 8  
||  
Db 4 MT 5

RESULT 75

Q8MEP0

ID Q8MEP0 PRELIMINARY; PRT; 11 AA.  
 AC Q8MEP0;  
 DT 01-OCT-2002 (TrEMBLrel. 22, Created)  
 DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)  
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)  
 DE Ribosomal protein 16 (Fragment).  
 GN RPL16.  
 OS Hibiscus peralbus.  
 OG Chloroplast.  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;  
 OC eurosids II; Malvales; Malvaceae; Malvoideae; Hibiscus.  
 OX NCBI\_TaxID=183256;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Pfeil B.E., Brubaker C.L., Craven L.A., Crisp M.D.;  
 RT "Phylogeny of Hibiscus and the tribe Hibisceae (Malvaceae) using  
 RT chloroplast DNA sequences of ndhF and the rpl16 intron."  
 RL Syst. Bot. 27:333-350(2002).  
 DR EMBL; AF384598; AAM50370.1; -.  
 DR GO; GO:0009507; C:chloroplast; IEA.  
 KW Chloroplast.  
 FT NON\_TER 1 1  
 FT NON\_TER 11 11  
 SQ SEQUENCE 11 AA; 1470 MW; 7227C351D32409D4 CRC64;

Query Match 18.2%; Score 2; DB 8; Length 11;  
 Best Local Similarity 100.0%; Pred. No. 1.2e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 RK 3  
 ||  
 Db 6 RK 7

Search completed: April 8, 2004, 15:46:11  
 Job time : 28.7692 secs

OM protein - protein search, using sw model

Run on: April 8, 2004, 15:30:07 ; Search time 5.15385 Seconds  
(without alignments)  
111.135 Million cell updates/sec

Title: US-09-787-443A-22  
Perfect score: 11  
Sequence: 1 ARKSRDMTAAK 11

Scoring table: OLIGO  
Gapop 60.0 , Gapext 60.0

Searched: 141681 seqs, 52070155 residues

Word size : 0

Total number of hits satisfying chosen parameters: 70

Minimum DB seq length: 11

Maximum DB seq length: 11

Post-processing: Listing first 100 summaries

Database : SwissProt\_42:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	3	27.3	11	1	UXB2_YEAST	P99013 saccharomyc
2	2	18.2	11	1	BRK_MEGFL	P12797 megascolia
3	2	18.2	11	1	CORZ_PERAM	P11496 periplaneta
4	2	18.2	11	1	CSI5_BACSU	P81095 bacillus su
5	2	18.2	11	1	ES1_RAT	P56571 rattus norv
6	2	18.2	11	1	NUHM_CANFA	P49820 canis famil
7	2	18.2	11	1	NXSN_PSETE	P59072 pseudonaja
8	2	18.2	11	1	PQQC_PSEFL	P55173 pseudomonas
9	2	18.2	11	1	Q2OA_COMTE	P80464 comamonas t
10	2	18.2	11	1	RR2_CONAM	P42341 conopholis
11	2	18.2	11	1	RS30_ONCMY	P83328 oncorhynchu
12	2	18.2	11	1	TIN4_HOPTI	P82654 hoplobatrac
13	1	9.1	11	1	ANGT_CRIGE	P09037 crinia geor
14	1	9.1	11	1	ASL1_BACSE	P83146 bacteroides
15	1	9.1	11	1	ASL2_BACSE	P83147 bacteroides
16	1	9.1	11	1	BPP3_BOTIN	P30423 bothrops in
17	1	9.1	11	1	BPP4_BOTIN	P30424 bothrops in

18	1	9.1	11	1	BPPB_AGKHA	P01021	agkistrodon
19	1	9.1	11	1	BPP_AGKHP	P04562	agkistrodon
20	1	9.1	11	1	CA21_LITCI	P82087	litoria cit
21	1	9.1	11	1	CA22_LITCI	P82088	litoria cit
22	1	9.1	11	1	CA31_LITCI	P82089	litoria cit
23	1	9.1	11	1	CA32_LITCI	P82090	litoria cit
24	1	9.1	11	1	CA41_LITCI	P82091	litoria cit
25	1	9.1	11	1	CA42_LITCI	P82092	litoria cit
26	1	9.1	11	1	CEP1_ACHFU	P22790	achatina fu
27	1	9.1	11	1	COXA_CANFA	P99501	canis famil
28	1	9.1	11	1	CX5A_CONAL	P58848	conus aulic
29	1	9.1	11	1	CX5B_CONAL	P58849	conus aulic
30	1	9.1	11	1	CXL1_CONMR	P58807	conus marmo
31	1	9.1	11	1	EFG_CLOPA	P81350	clostridium
32	1	9.1	11	1	FAR6_PENMO	P83321	penaeus mon
33	1	9.1	11	1	FAR9_CALVO	P41864	calliphora
34	1	9.1	11	1	HS70_PINPS	P81672	pinus pinas
35	1	9.1	11	1	LADD_ONCMY	P81018	oncorhynch
36	1	9.1	11	1	LPW_THETH	P05624	thermus the
37	1	9.1	11	1	LSK1_LEUMA	P04428	leucophaea
38	1	9.1	11	1	LSKP_PERAM	P36885	periplaneta
39	1	9.1	11	1	MHBI_KLEPN	P80580	klebsiella
40	1	9.1	11	1	MLG_THETS	P41989	theromyzon
41	1	9.1	11	1	MORN_HUMAN	P01163	homo sapien
42	1	9.1	11	1	OAIF_SARBU	P83518	sarcophaga
43	1	9.1	11	1	PKC1_CARMO	P82684	carausius m
44	1	9.1	11	1	PVK1_PERAM	P41837	periplaneta
45	1	9.1	11	1	RANC_RANPI	P08951	rana pipien
46	1	9.1	11	1	RE41_LITRU	P82074	litoria rub
47	1	9.1	11	1	RRPL_CHAV	P13179	chandipura
48	1	9.1	11	1	T2P1_PROVU	P31031	proteus vul
49	1	9.1	11	1	TIN1_HOPTI	P82651	hoplobatr
50	1	9.1	11	1	TKC2_CALVO	P41518	calliphora
51	1	9.1	11	1	TKN1_PSEGU	P42986	pseudophryn
52	1	9.1	11	1	TKN1_UPEIN	P82026	uperoleia i
53	1	9.1	11	1	TKN1_UPERU	P08612	uperoleia r
54	1	9.1	11	1	TKN2_PSEGU	P42987	pseudophryn
55	1	9.1	11	1	TKN2_UPERU	P08616	uperoleia r
56	1	9.1	11	1	TKN3_PSEGU	P42988	pseudophryn
57	1	9.1	11	1	TKN4_PSEGU	P42989	pseudophryn
58	1	9.1	11	1	TKN5_PSEGU	P42990	pseudophryn
59	1	9.1	11	1	TKNA_CHICK	P19850	gallus gall
60	1	9.1	11	1	TKNA_GADMO	P28498	gadus morhu
61	1	9.1	11	1	TKNA_HORSE	P01290	equus cabal
62	1	9.1	11	1	TKNA_ONCMY	P28499	oncorhynch
63	1	9.1	11	1	TKNA_RANCA	P22688	rana catesb
64	1	9.1	11	1	TKNA_RANRI	P29207	rana ridibu
65	1	9.1	11	1	TKNA_SCYCA	P41333	scyliorhinu
66	1	9.1	11	1	TKND_RANCA	P22691	rana catesb
67	1	9.1	11	1	TKN_ELEMO	P01293	eledone mos
68	1	9.1	11	1	TKN_PHYFU	P08615	physalaemus
69	1	9.1	11	1	UF05_MOUSE	P38643	mus musculu
70	1	9.1	11	1	ULAG_HUMAN	P31933	homo sapien

# ALIGNMENTS



RESULT 1

UXB2\_YEAST

ID UXB2\_YEAST STANDARD; PRT; 11 AA.  
 AC P99013;  
 DT 01-NOV-1995 (Rel. 32, Created)  
 DT 01-NOV-1995 (Rel. 32, Last sequence update)  
 DT 15-MAR-2004 (Rel. 43, Last annotation update)  
 DE Unknown protein from 2D-page (Spot 2D-000K2F) (Fragment).  
 OS Saccharomycès cerevisiae (Baker's yeast).  
 OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;  
 OC Saccharomycetales; Saccharomycetaceae; Saccharomyces.  
 OX NCBI\_TaxID=4932;  
 RN [1]  
 RP SEQUENCE.  
 RC STRAIN=X2180-1A;  
 RA Sanchez J.-C., Golaz O., Schaller D., Morch F., Frutiger S.,  
 RA Hughes G.J., Appel R.D., Deshusses J., Hochstrasser D.F.;  
 RL Submitted (AUG-1995) to Swiss-Prot.  
 CC -!- MISCELLANEOUS: On the 2D-gel the determined pI of this unknown  
 CC protein is: 6.20, its MW is: 9.2 kDa.  
 DR SWISS-2DPAGE; P99013; YEAST.  
 FT NON\_TER 11 11  
 SQ SEQUENCE 11 AA; 1328 MW; EC38021C0DCB42DA CRC64;

Query Match 27.3%; Score 3; DB 1; Length 11;  
 Best Local Similarity 100.0%; Pred. No. 9.4e+02;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ARK 3  
 |||  
 Db 7 ARK 9

RESULT 2

BRK\_MEGFL

ID BRK\_MEGFL STANDARD; PRT; 11 AA.  
 AC P12797;  
 DT 01-OCT-1989 (Rel. 12, Created)  
 DT 01-OCT-1989 (Rel. 12, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE Megascoliakinin ([Thr6]bradykinin-Lys-Ala) [Contains: Bradykinin-like  
 DE peptide ([Thr6]bradykinin)].  
 OS Megascolia flavifrons (Garden dagger wasp) (Solitary wasp).  
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
 OC Neoptera; Endopterygota; Hymenoptera; Apocrita; Aculeata; Vespoidea;  
 OC Scoliidae; Megascolia.  
 OX NCBI\_TaxID=7437;  
 RN [1]  
 RP SEQUENCE.  
 RC TISSUE=Venom;  
 RX MEDLINE=87293024; PubMed=3617088;  
 RA Yasuhara T., Mantel P., Nakajima T., Piek T.;  
 RT "Two kinins isolated from an extract of the venom reservoirs of the  
 RT solitary wasp Megascolia flavifrons."  
 RL Toxicon 25:527-535(1987).  
 RN [2]

RP SEQUENCE.  
 RC TISSUE=Venom;  
 RA Nakajima T., Piek T., Yashuara T., Mantel P.;  
 RT "Two kinins isolated from the venom of *Megascolia flavifrons*.";  
 RL Toxicon 26:34-34(1988).  
 CC -!- FUNCTION: Both proteins have bradykinin-like, although lower  
 CC activities (e.g. smooth muscle contraction).  
 CC -!- SUBCELLULAR LOCATION: Secreted; wasp venom reservoirs.  
 CC -!- SIMILARITY: Belongs to the bradykinin family.  
 DR PIR; B26744; B26744.  
 DR GO; GO:0005615; C:extracellular space; IDA.  
 DR GO; GO:0045776; P:negative regulation of blood pressure; ISS.  
 DR GO; GO:0045987; P:positive regulation of smooth muscle contra. . .; TAS.  
 KW Bradykinin; Vasodilator.  
 FT PEPTIDE 1 11 MEGASCOLIAKININ.  
 FT PEPTIDE 1 9 BRADYKININ-LIKE PEPTIDE.  
 SQ SEQUENCE 11 AA; 1273 MW; 33867393D771A9C8 CRC64;

Query Match 18.2%; Score 2; DB 1; Length 11;  
 Best Local Similarity 100.0%; Pred. No. 1.2e+04;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 RK 3  
 ||  
 Db 9 RK 10

### RESULT 3

CORZ\_PERAM  
 ID CORZ\_PERAM STANDARD; PRT; 11 AA.  
 AC P11496;  
 DT 01-OCT-1989 (Rel. 12, Created)  
 DT 01-FEB-1994 (Rel. 28, Last sequence update)  
 DT 10-OCT-2003 (Rel. 42, Last annotation update)  
 DE Corazonin.  
 OS *Periplaneta americana* (American cockroach).  
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
 OC Neoptera; Orthopteroidea; Dictyoptera; Blattaria; Blattoidea;  
 OC Blattellidae; Periplaneta.  
 OX NCBI\_TaxID=6978;  
 RN [1]  
 RP SEQUENCE.  
 RC TISSUE=Corpora cardiaca;  
 RX MEDLINE=89325572; PubMed=2753132;  
 RA Veenstra J.A.;  
 RT "Isolation and structure of corazonin, a cardioactive peptide from  
 RT the American cockroach.";  
 RL FEBS Lett. 250:231-234(1989).  
 CC -!- FUNCTION: Cardioactive peptide. Corazonin is probably involved  
 CC in the physiological regulation of the heart beat.  
 CC -!- SUBCELLULAR LOCATION: Secreted.  
 DR PIR; S05002; S05002.  
 KW Neuropeptide; Amidation; Pyrrolidone carboxylic acid.  
 FT MOD\_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.  
 FT MOD\_RES 11 11 AMIDATION.  
 SQ SEQUENCE 11 AA; 1387 MW; C7CFF32D6415AB46 CRC64;

Query Match 18.2%; Score 2; DB 1; Length 11;  
Best Local Similarity 100.0%; Pred. No. 1.2e+04;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 SR 5  
||  
Db 6 SR 7

RESULT 4

CSI5\_BACSU

ID CSI5\_BACSU STANDARD; PRT; 11 AA.  
AC P81095;  
DT 15-JUL-1998 (Rel. 36, Created)  
DT 15-JUL-1998 (Rel. 36, Last sequence update)  
DT 28-FEB-2003 (Rel. 41, Last annotation update)  
DE Cold shock protein CSI5 (11 kDa cold shock protein) (Fragment).  
OS Bacillus subtilis.  
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.  
OX NCBI\_TaxID=1423;  
RN [1]  
RP SEQUENCE.  
RC STRAIN=168 / JH642;  
RA Graumann P.L., Schmid R., Marahiel M.A.;  
RL Submitted (OCT-1997) to Swiss-Prot.  
RN [2]  
RP CHARACTERIZATION.  
RC STRAIN=168 / JH642;  
RX MEDLINE=96345629; PubMed=8755892;  
RA Graumann P., Schroeder K., Schmid R., Marahiel M.A.;  
RT "Cold shock stress-induced proteins in Bacillus subtilis."  
RL J. Bacteriol. 178:4611-4619(1996).  
CC -!- SUBCELLULAR LOCATION: Cytoplasmic.  
CC -!- INDUCTION: In response to low temperature.  
CC -!- CAUTION: Could not be found in the genome of B.subtilis 168.  
FT NON\_TER 11 11  
SQ SEQUENCE 11 AA; 1360 MW; 15F6ECEE6322C330 CRC64;

Query Match 18.2%; Score 2; DB 1; Length 11;  
Best Local Similarity 100.0%; Pred. No. 1.2e+04;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 10 IK 11  
||  
Db 4 IK 5

RESULT 5

ES1\_RAT

ID ES1\_RAT STANDARD; PRT; 11 AA.  
AC P56571;  
DT 15-DEC-1998 (Rel. 37, Created)  
DT 15-DEC-1998 (Rel. 37, Last sequence update)  
DT 15-MAR-2004 (Rel. 43, Last annotation update)  
DE ES1 protein, mitochondrial (Fragment).  
OS Rattus norvegicus (Rat).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
 OX NCBI\_TaxID=10116;  
 RN [1]  
 RP SEQUENCE.  
 RC STRAIN=Wistar; TISSUE=Heart;  
 RA Li X.-P., Pleissner K.-P., Scheler C., Regitz-Zagrosek V., Salikov J.,  
 RA Jungblut P.R.;  
 RL Submitted (SEP-1998) to Swiss-Prot.  
 CC -!- SUBCELLULAR LOCATION: Mitochondrial (Potential).  
 CC -!- MISCELLANEOUS: By 2D-PAGE, the determined pI of this protein (spot  
 CC P2) is: 8.9, its MW is: 25 kDa.  
 CC -!- SIMILARITY: BELONGS TO THE ES1 FAMILY.  
 KW Mitochondrion.  
 FT NON\_TER 11 11  
 SQ SEQUENCE 11 AA; 1142 MW; D862272D32C72DC2 CRC64;

Query Match 18.2%; Score 2; DB 1; Length 11;  
 Best Local Similarity 100.0%; Pred. No. 1.2e+04;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AR 2  
 ||  
 Db 2 AR 3

# RESULT 6

## NUHM\_CANFA

ID NUHM\_CANFA STANDARD; PRT; 11 AA.  
 AC P49820;  
 DT 01-OCT-1996 (Rel. 34, Created)  
 DT 15-JUL-1998 (Rel. 36, Last sequence update)  
 DT 10-OCT-2003 (Rel. 42, Last annotation update)  
 DE NADH-ubiquinone oxidoreductase 24 kDa subunit (EC 1.6.5.3)  
 DE (EC 1.6.99.3) (Fragment).  
 GN NDUFV2.  
 OS Canis familiaris (Dog).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.  
 OX NCBI\_TaxID=9615;  
 RN [1]  
 RP SEQUENCE.  
 RC TISSUE=Heart;  
 RX MEDLINE=98163340; PubMed=9504812;  
 RA Dunn M.J., Corbett J.M., Wheeler C.H.;  
 RT "HSC-2DPAGE and the two-dimensional gel electrophoresis database of  
 RT dog heart proteins.";  
 RL Electrophoresis 18:2795-2802(1997).  
 CC -!- FUNCTION: TRANSFER OF ELECTRONS FROM NADH TO THE RESPIRATORY  
 CC CHAIN. THE IMMEDIATE ELECTRON ACCEPTOR FOR THE ENZYME IS BELIEVED  
 CC TO BE UBIQUINONE. COMPONENT OF THE FLAVOPROTEIN-SULFUR (FP)  
 CC FRAGMENT OF THE ENZYME.  
 CC -!- CATALYTIC ACTIVITY: NADH + ubiquinone = NAD(+) + ubiquinol.  
 CC -!- CATALYTIC ACTIVITY: NADH + acceptor = NAD(+) + reduced acceptor.  
 CC -!- COFACTOR: Binds 1 2Fe-2S cluster (Potential).  
 CC -!- SUBUNIT: Mammalian complex I is composed of 45 different subunits.  
 CC -!- SUBCELLULAR LOCATION: Matrix and cytoplasmic side of the  
 CC mitochondrial inner membrane.

CC -!- SIMILARITY: Belongs to the complex I 24 kDa subunit family.  
 DR HSC-2DPAGE; P49820; DOG.  
 DR InterPro; IPR002023; Cmplx1\_24kDa.  
 DR PROSITE; PS01099; COMPLEX1\_24K; PARTIAL.  
 KW Oxidoreductase; NAD; Ubiquinone; Mitochondrion; Metal-binding;  
 KW Iron-sulfur; Iron; 2Fe-2S.  
 FT NON\_TER 11 11  
 SQ SEQUENCE 11 AA; 1099 MW; 267F5369C9C72DD8 CRC64;

Query Match 18.2%; Score 2; DB 1; Length 11;  
 Best Local Similarity 100.0%; Pred. No. 1.2e+04;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 RD 6  
 ||  
 Db 10 RD 11

# RESULT 7

NXSN\_PSETE  
 ID NXSN\_PSETE STANDARD; PRT; 11 AA.  
 AC P59072;  
 DT 28-FEB-2003 (Rel. 41, Created)  
 DT 28-FEB-2003 (Rel. 41, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE Short neurotoxin N1 (Alpha neurotoxin) (Fragment).  
 OS Pseudonaja textilis (Eastern brown snake).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;  
 OC Elapidae; Acanthophiinae; Pseudonaja.  
 OX NCBI\_TaxID=8673;  
 RN [1]  
 RP SEQUENCE, AND MASS SPECTROMETRY.  
 RC TISSUE=Venom;  
 RX MEDLINE=99449602; PubMed=10518793;  
 RA Gong N.L., Armugam A., Jeyaseelan K.;  
 RT "Postsynaptic short-chain neurotoxins from Pseudonaja textilis: cDNA  
 cloning, expression and protein characterization."  
 RL Eur. J. Biochem. 265:982-989(1999).  
 CC -!- FUNCTION: Lethal neurotoxin, binds and inhibits nicotinic  
 CC acetylcholine receptors (nAChR).  
 CC -!- SUBCELLULAR LOCATION: Secreted.  
 CC -!- TISSUE SPECIFICITY: Expressed by the venom gland.  
 CC -!- MASS SPECTROMETRY: MW=6236; METHOD=Electrospray.  
 CC -!- MISCELLANEOUS: LD(50) is 0.84 mg/kg by intravenous injection.  
 CC -!- SIMILARITY: Belongs to the snake toxin family.  
 DR InterPro; IPR003571; Snake\_toxin.  
 DR PROSITE; PS00272; SNAKE\_TOXIN; PARTIAL.  
 KW Toxin; Neurotoxin; Postsynaptic neurotoxin;  
 KW Acetylcholine receptor inhibitor; Multigene family.  
 FT UNSURE 3 3  
 FT NON\_TER 11 11  
 SQ SEQUENCE 11 AA; 1319 MW; 0D1EF0C81B58732B CRC64;

Query Match 18.2%; Score 2; DB 1; Length 11;  
 Best Local Similarity 100.0%; Pred. No. 1.2e+04;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 RD 6  
||  
Db 8 RD 9

RESULT 8

PQQC\_PSEFL

ID PQQC\_PSEFL STANDARD; PRT; 11 AA.  
AC P55173;  
DT 01-OCT-1996 (Rel. 34, Created)  
DT 01-OCT-1996 (Rel. 34, Last sequence update)  
DT 10-OCT-2003 (Rel. 42, Last annotation update)  
DE Coenzyme PQQ synthesis protein C (Pyrroloquinoline quinone  
DE biosynthesis protein C) (Fragment).  
GN PQQC.  
OS Pseudomonas fluorescens.  
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;  
OC Pseudomonadaceae; Pseudomonas.  
OX NCBI\_TaxID=294;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=CHA0;  
RX MEDLINE=96064397; PubMed=8526497;  
RA Schnider U., Keel C., Defago G., Haas D.;  
RT "Tn5-directed cloning of pqq genes from Pseudomonas fluorescens CHA0:  
RT mutational inactivation of the genes results in overproduction of the  
RT antibiotic pyoluteorin."  
RL Appl. Environ. Microbiol. 61:3856-3864(1995).  
CC -!- PATHWAY: Pyrroloquinoline quinone (PQQ) biosynthesis.  
CC -!- SIMILARITY: Belongs to the pqqC family.  
CC -----  
CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
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CC use by non-profit institutions as long as its content is in no way  
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CC -----  
DR EMBL; X87299; CAA60734.1; -.  
DR PIR; S58244; S58244.  
DR HAMAP; MF\_00654; -; 1.  
KW PQQ biosynthesis.  
FT NON\_TER 11 11  
SQ SEQUENCE 11 AA; 1182 MW; 89DF46E4C5B73771 CRC64;

Query Match 18.2%; Score 2; DB 1; Length 11;  
Best Local Similarity 100.0%; Pred. No. 1.2e+04;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 MT 8  
||  
Db 1 MT 2

RESULT 9

## Q20A\_COMTE

ID Q20A\_COMTE STANDARD; PRT; 11 AA.  
 AC P80464;  
 DT 01-NOV-1995 (Rel. 32, Created)  
 DT 01-NOV-1995 (Rel. 32, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE Quinoline 2-oxidoreductase, alpha chain (EC 1.3.99.17) (Fragment).  
 OS Comamonas testosteroni (Pseudomonas testosteroni).  
 OC Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;  
 OC Comamonadaceae; Comamonas.  
 OX NCBI\_TaxID=285;  
 RN [1]  
 RP SEQUENCE.  
 RC STRAIN=63;  
 RX MEDLINE=96035889; PubMed=7556204;  
 RA Schach S., Tshisuaka B., Fetzner S., Lingens F.;  
 RT "Quinoline 2-oxidoreductase and 2-oxo-1,2-dihydroquinoline 5,6-  
 RT dioxygenase from Comamonas testosteroni 63. The first two enzymes in  
 RT quinoline and 3-methylquinoline degradation.";  
 RL Eur. J. Biochem. 232:536-544(1995).  
 CC -!- FUNCTION: Converts (3-methyl-)-quinoline to (3-methyl-)2-oxo-  
 CC 1,2-dihydroquinoline.  
 CC -!- CATALYTIC ACTIVITY: Quinoline + acceptor + H(2)O = isoquinolin-  
 CC 1(2H)-one + reduced acceptor.  
 CC -!- COFACTOR: FAD, molybdenum and iron-sulfur.  
 CC -!- PATHWAY: Degradation of quinoline and (3-methyl-)quinoline; first  
 CC step.  
 CC -!- SUBUNIT: Heterohexamer of two alpha chains, two beta chains, and  
 CC two gamma chains (Probable).  
 DR PIR; S66606; S66606.  
 KW Oxidoreductase; Flavoprotein; FAD; Molybdenum.  
 FT NON\_TER 11 11  
 SQ SEQUENCE 11 AA; 1213 MW; 869094322B1DC2CA CRC64;

Query Match 18.2%; Score 2; DB 1; Length 11;  
 Best Local Similarity 100.0%; Pred. No. 1.2e+04;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 KS 4  
 ||  
 Db 2 KS 3

## RESULT 10

## RR2\_CONAM

ID RR2\_CONAM STANDARD; PRT; 11 AA.  
 AC P42341;  
 DT 01-NOV-1995 (Rel. 32, Created)  
 DT 01-NOV-1995 (Rel. 32, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE Chloroplast 30S ribosomal protein S2 (Fragment).  
 GN RPS2.  
 OS Conopholis americana (Squawroot).  
 OG Chloroplast.  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;  
 OC lamiids; Lamiales; Orobanchaceae; Orobancheae; Conopholis.

OX NCBI\_TaxID=4179;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=92145776; PubMed=1723664;  
 RA Taylor G., Wolfe K.H., Morden C.W., Depamphilis C.W., Palmer J.D.;  
 RT "Lack of a functional plastid tRNA(Cys) gene is associated with loss  
 of photosynthesis in a lineage of parasitic plants.";  
 RL Curr. Genet. 20:515-518(1991).  
 CC -!- SIMILARITY: Belongs to the S2P family of ribosomal proteins.  
 CC -----  
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
 CC the European Bioinformatics Institute. There are no restrictions on its  
 CC use by non-profit institutions as long as its content is in no way  
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 CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC -----  
 DR EMBL; X64567; CAA45868.1; -.  
 DR PIR; S32575; S32575.  
 DR HAMAP; MF\_00291; -; 1.  
 DR InterPro; IPR001865; Ribosomal\_S2.  
 DR PROSITE; PS00962; RIBOSOMAL\_S2\_1; PARTIAL.  
 DR PROSITE; PS00963; RIBOSOMAL\_S2\_2; PARTIAL.  
 KW Ribosomal protein; Chloroplast.  
 FT NON\_TER 11 11  
 SQ SEQUENCE 11 AA; 1497 MW; 76CD719954536B44 CRC64;

Query Match 18.2%; Score 2; DB 1; Length 11;  
 Best Local Similarity 100.0%; Pred. No. 1.2e+04;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 MT 8  
 ||  
 Db 1 MT 2

RESULT 11  
 RS30\_ONCMY  
 ID RS30\_ONCMY STANDARD; PRT; 11 AA.  
 AC P83328;  
 DT 28-FEB-2003 (Rel. 41, Created)  
 DT 28-FEB-2003 (Rel. 41, Last sequence update)  
 DT 10-OCT-2003 (Rel. 42, Last annotation update)  
 DE 40S ribosomal protein S30 (Fragment).  
 GN FAU.  
 OS Oncorhynchus mykiss (Rainbow trout) (Salmo gairdneri).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;  
 OC Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.  
 OX NCBI\_TaxID=8022;  
 RN [1]  
 RP SEQUENCE, FUNCTION, AND MASS SPECTROMETRY.  
 RC TISSUE=Skin mucus;  
 RX MEDLINE=22142142; PubMed=12147245;  
 RA Fernandes J.M.O., Smith V.J.;  
 RT "A novel antimicrobial function for a ribosomal peptide from rainbow



RT trout skin.";  
 RL Biochem. Biophys. Res. Commun. 296:167-171(2002).  
 CC -!- FUNCTION: Has antibacterial activity against Gram-positive  
 CC bacteria.  
 CC -!- MASS SPECTROMETRY: MW=6676.6; METHOD=MALDI.  
 CC -!- SIMILARITY: Belongs to the S30E family of ribosomal proteins.  
 KW Ribosomal protein; Antibiotic.  
 FT NON\_TER 11 11  
 SQ SEQUENCE 11 AA; 1123 MW; 2312AB630DD735B8 CRC64;

Query Match 18.2%; Score 2; DB 1; Length 11;  
 Best Local Similarity 100.0%; Pred. No. 1.2e+04;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AR 2  
 ||  
 Db 7 AR 8

# RESULT 12

## TIN4\_HOPTI

ID TIN4\_HOPTI STANDARD; PRT; 11 AA.  
 AC P82654;  
 DT 16-OCT-2001 (Rel. 40, Created)  
 DT 16-OCT-2001 (Rel. 40, Last sequence update)  
 DT 10-OCT-2003 (Rel. 42, Last annotation update)  
 DE Tigerinin-4.  
 OS Hoplobatrachus tigerinus (Indian bull frog) (Rana tigerina).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Ranidae;  
 OC Hoplobatrachus.  
 OX NCBI\_TaxID=103373;  
 RN [1]  
 RP SEQUENCE, FUNCTION, MASS SPECTROMETRY, AND DISULFIDE BONDS.  
 RC TISSUE=Skin secretion;  
 RX PubMed=11031261;  
 RA Purna Sai K., Jaganadham M.V., Vairamani M., Raju N.P.,  
 RA Devi A.S., Nagaraj R., Sitaram N.;  
 RT "Tigerinins: novel antimicrobial peptides from the Indian frog Rana  
 RT tigerina.";  
 RL J. Biol. Chem. 276:2701-2707(2001).  
 CC -!- FUNCTION: Antibacterial activity against B.subtilis, E.coli,  
 CC S.aureus, M.luteus, P.putida and S.cerevisiae.  
 CC -!- SUBCELLULAR LOCATION: Secreted.  
 CC -!- TISSUE SPECIFICITY: Skin.  
 CC -!- MASS SPECTROMETRY: MW=1247; METHOD=MALDI.  
 KW Amphibian defense peptide; Antibiotic.  
 FT DISULFID 3 11  
 SQ SEQUENCE 11 AA; 1248 MW; 117D8EFD37605DCB CRC64;

Query Match 18.2%; Score 2; DB 1; Length 11;  
 Best Local Similarity 100.0%; Pred. No. 1.2e+04;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 AI 10  
 ||  
 Db 5 AI 6

# RESULT 13

## ANGT\_CRIGE

ID ANGT\_CRIGE STANDARD; PRT; 11 AA.  
AC P09037;  
DT 01-NOV-1988 (Rel. 09, Created)  
DT 01-NOV-1988 (Rel. 09, Last sequence update)  
DT 10-OCT-2003 (Rel. 42, Last annotation update)  
DE Crinia-angiotensin II.  
OS Crinia georgiana (Quacking frog).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Amphibia; Batrachia; Anura; Neobatrachia; Hyloidea; Myobatrachidae;  
OC Myobatrachinae; Crinia.  
OX NCBI\_TaxID=8374;  
RN [1]  
RP SEQUENCE.  
RC TISSUE=Skin secretion;  
RX MEDLINE=80024575; PubMed=488254;  
RA Erspamer V., Melchiorri P., Nakajima T., Yasuhara T., Endean R.;  
RT "Amino acid composition and sequence of crinia-angiotensin, an  
RT angiotensin II-like endecapeptide from the skin of the Australian  
RT frog Crinia georgiana.";  
RL Experientia 35:1132-1133(1979).  
CC -!- SUBCELLULAR LOCATION: Secreted.  
CC -!- TISSUE SPECIFICITY: Skin.  
DR PIR; S07207; S07207.  
KW Vasoconstrictor.  
SQ SEQUENCE 11 AA; 1271 MW; 8A0921F7DB50440A CRC64;

Query Match 9.1%; Score 1; DB 1; Length 11;  
Best Local Similarity 100.0%; Pred. No. 9.8e+04;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 A 1  
|  
Db 1 A 1

# RESULT 14

## ASL1\_BACSE

ID ASL1\_BACSE STANDARD; PRT; 11 AA.  
AC P83146;  
DT 28-FEB-2003 (Rel. 41, Created)  
DT 28-FEB-2003 (Rel. 41, Last sequence update)  
DT 28-FEB-2003 (Rel. 41, Last annotation update)  
DE Acharan sulfate lyase 1 (EC 4.2.2.-) (Fragment).  
OS Bacteroides stercoris.  
OC Bacteria; Bacteroidetes; Bacteroides (class); Bacteroidales;  
OC Bacteroidaceae; Bacteroides.  
OX NCBI\_TaxID=46506;  
RN [1]  
RP SEQUENCE, FUNCTION, ENZYME REGULATION, AND SUBUNIT.  
RC STRAIN=HJ-15;  
RX MEDLINE=21223019; PubMed=11322884;  
RA Kim B.-T., Hong S.-W., Kim W.-S., Kim Y.S., Kim D.-H.;  
RT "Purification and characterization of acharan sulfate lyases, two

RT novel heparinases, from *Bacteroides stercoris* HJ-15.";  
 RL Eur. J. Biochem. 268:2635-2641(2001).  
 CC -!- FUNCTION: Degrades acharan sulfate and, to a lesser extent,  
 CC heparin and heparan sulfate.  
 CC -!- ENZYME REGULATION: Inhibited by cupric ion, nitrogen and cobalt.  
 CC Activated by reducing agents, such as DL-dithiothreitol and 2-  
 CC mercaptoethanol.  
 CC -!- SUBUNIT: Monomer.  
 CC -!- PTM: The N-terminus is blocked.  
 CC -!- MISCELLANEOUS: Has an isoelectric point of 8.6. Its optimum pH is  
 CC 7.2 and optimum temperature 45 degrees Celsius.  
 KW Lyase; Heparin-binding.  
 FT NON\_TER 1 1  
 FT NON\_TER 11 11  
 SQ SEQUENCE 11 AA; 1395 MW; 01B2DAA241E865AB CRC64;

Query Match 9.1%; Score 1; DB 1; Length 11;  
 Best Local Similarity 100.0%; Pred. No. 9.8e+04;  
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 10 I 10  
 |  
 Db 3 I 3

# RESULT 15

## ASL2\_BACSE

ID ASL2\_BACSE STANDARD; PRT; 11 AA.  
 AC P83147;  
 DT 28-FEB-2003 (Rel. 41, Created)  
 DT 28-FEB-2003 (Rel. 41, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE Acharan sulfate lyase 2 (EC 4.2.2.-) (Fragment).  
 OS *Bacteroides stercoris*.  
 OC Bacteria; Bacteroidetes; *Bacteroides* (class); Bacteroidales;  
 OC Bacteroidaceae; *Bacteroides*.  
 OX NCBI\_TaxID=46506;  
 RN [1]  
 RP SEQUENCE, FUNCTION, ENZYME REGULATION, AND SUBUNIT.  
 RC STRAIN=HJ-15;  
 RX MEDLINE=21223019; PubMed=11322884;  
 RA Kim B.-T., Hong S.-W., Kim W.-S., Kim Y.S., Kim D.-H.;  
 RT "Purification and characterization of acharan sulfate lyases, two  
 RT novel heparinases, from *Bacteroides stercoris* HJ-15.";  
 RL Eur. J. Biochem. 268:2635-2641(2001).  
 CC -!- FUNCTION: Degrades acharan sulfate and, to a lesser extent,  
 CC heparin and heparan sulfate.  
 CC -!- ENZYME REGULATION: Inhibited by cupric ion, nitrogen and lead.  
 CC Activated by reducing agents, such as DL-dithiothreitol and 2-  
 CC mercaptoethanol.  
 CC -!- SUBUNIT: Monomer.  
 CC -!- PTM: The N-terminus is blocked.  
 CC -!- MISCELLANEOUS: Has an isoelectric point of 8.6. Its optimum pH is  
 CC 7.2 and optimum temperature 45 degrees Celsius.  
 KW Lyase; Heparin-binding.  
 FT NON\_TER 1 1  
 FT NON\_TER 11 11

SQ SEQUENCE 11 AA; 1195 MW; D79D897C7AA451AD CRC64;

Query Match 9.1%; Score 1; DB 1; Length 11;  
Best Local Similarity 100.0%; Pred. No. 9.8e+04;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 T 8  
|  
Db 1 T 1

RESULT 16

BPP3\_BOTIN

ID BPP3\_BOTIN STANDARD; PRT; 11 AA.

AC P30423;

DT 01-APR-1993 (Rel. 25, Created)

DT 01-FEB-1994 (Rel. 28, Last sequence update)

DT 28-FEB-2003 (Rel. 41, Last annotation update)

DE Bradykinin-potentiating peptide S4,3,2 (10C) (Angiotensin-converting enzyme inhibitor).

OS Bothrops insularis (Island jararaca) (Queimada jararaca).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;

OC Viperidae; Crotalinae; Bothrops.

OX NCBI\_TaxID=8723;

RN [1]

RP SEQUENCE.

RC TISSUE=Venom;

RX MEDLINE=90351557; PubMed=2386615;

RA Cintra A.C.O., Vieira C.A., Giglio J.R.;

RT "Primary structure and biological activity of bradykinin potentiating peptides from Bothrops insularis snake venom.";

RL J. Protein Chem. 9:221-227(1990).

CC -!- FUNCTION: This peptide both inhibits the activity of the  
CC angiotensin-converting enzyme and enhances the action of  
CC bradykinin by inhibiting the kinases that inactivate it.  
CC It acts as an indirect hypotensive agent.

DR PIR; C37196; C37196.

KW Hypotensive agent; Pyrrolidone carboxylic acid.

FT MOD RES 1 1 PYRROLIDONE CARBOXYLIC ACID.

SQ SEQUENCE 11 AA; 1199 MW; 20B25813C7741777 CRC64;

Query Match 9.1%; Score 1; DB 1; Length 11;  
Best Local Similarity 100.0%; Pred. No. 9.8e+04;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 R 2  
|  
Db 6 R 6

RESULT 17

BPP4\_BOTIN

ID BPP4\_BOTIN STANDARD; PRT; 11 AA.

AC P30424;

DT 01-APR-1993 (Rel. 25, Created)

DT 01-FEB-1994 (Rel. 28, Last sequence update)

DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE Bradykinin-potentiating peptide S4,1,2 (Angiotensin-converting  
 DE enzyme inhibitor).  
 OS Bothrops insularis (Island jararaca) (Queimada jararaca).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;  
 OC Viperidae; Crotalinae; Bothrops.  
 OX NCBI\_TaxID=8723;  
 RN [1]  
 RP SEQUENCE.  
 RC TISSUE=Venom;  
 RX MEDLINE=90351557; PubMed=2386615;  
 RA Cintra A.C.O., Vieira C.A., Giglio J.R.;  
 RT "Primary structure and biological activity of bradykinin potentiating  
 RT peptides from Bothrops insularis snake venom."  
 RL J. Protein Chem. 9:221-227(1990).  
 CC -!- FUNCTION: This peptide both inhibits the activity of the  
 CC angiotensin-converting enzyme and enhances the action of  
 CC bradykinin by inhibiting the kinases that inactivate it.  
 CC It acts as an indirect hypotensive agent.  
 DR PIR; D37196; D37196.  
 KW Hypotensive agent; Pyrrolidone carboxylic acid.  
 FT MOD\_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.  
 SQ SEQUENCE 11 AA; 1143 MW; 20BBBF13C7741777 CRC64;

Query Match 9.1%; Score 1; DB 1; Length 11;  
 Best Local Similarity 100.0%; Pred. No. 9.8e+04;  
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 R 2  
 |  
 Db 6 R 6

# RESULT 18

BPPB\_AGKHA

ID BPPB\_AGKHA STANDARD; PRT; 11 AA.

AC P01021;

DT 21-JUL-1986 (Rel. 01, Created)

DT 01-FEB-1994 (Rel. 28, Last sequence update)

DT 28-FEB-2003 (Rel. 41, Last annotation update)

DE Bradykinin-potentiating peptide B (Angiotensin-converting

DE enzyme inhibitor).

OS Agkistrodon halys blomhoffii (Mamushi) (Gloydus blomhoffii).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;

OC Viperidae; Crotalinae; Gloydus.

OX NCBI\_TaxID=242054;

RN [1]

RP SEQUENCE.

RC TISSUE=Venom;

RA Kato H., Suzuki T.;

RT "Amino acid sequence of bradykinin-potentiating peptide isolated from

RT the venom of Agkistrodon halys blomhoffii.";

RL Proc. Jpn. Acad., B, Phys. Biol. Sci. 46:176-181(1970).

CC -!- FUNCTION: This peptide both inhibits the activity of the

CC angiotensin-converting enzyme and enhances the action of

CC bradykinin by inhibiting the kinases that inactivate it.  
CC It acts as an indirect hypotensive agent.  
DR PIR; A01254; XASNBA.  
KW Hypotensive agent; Pyrrolidone carboxylic acid.  
FT MOD\_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.  
SQ SEQUENCE 11 AA; 1199 MW; 295CBF0627741777 CRC64;

Query Match 9.1%; Score 1; DB 1; Length 11;  
Best Local Similarity 100.0%; Pred. No. 9.8e+04;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 R 2  
|  
Db 6 R 6

#### RESULT 19

##### BPP\_AGKHP

ID BPP\_AGKHP STANDARD; PRT; 11 AA.  
AC P04562;  
DT 13-AUG-1987 (Rel. 05, Created)  
DT 01-FEB-1994 (Rel. 28, Last sequence update)  
DT 28-FEB-2003 (Rel. 41, Last annotation update)  
DE Bradykinin-potentiating peptide (Angiotensin-converting  
DE enzyme inhibitor).  
OS Agkistrodon halys pallas (Chinese water moccasin) (Gloydus halys  
OS pallas).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;  
OC Viperidae; Crotalinae; Gloydus.  
OX NCBI\_TaxID=8714;  
RN [1]  
RP SEQUENCE.  
RC TISSUE=Venom;  
RX MEDLINE=86177022; PubMed=3008123;  
RA Chi C.-W., Wang S.-Z., Xu L.-G., Wang M.-Y., Lo S.-S., Huang W.-D.;  
RT "Structure-function studies on the bradykinin potentiating peptide  
RT from Chinese snake venom (Agkistrodon halys pallas).";  
RL Peptides 6 Suppl. 3:339-342(1985).  
CC -!- FUNCTION: This peptide both inhibits the activity of the  
CC angiotensin-converting enzyme and enhances the action of  
CC bradykinin by inhibiting the kinases that inactivate it.  
CC It acts as an indirect hypotensive agent.  
DR PIR; JC0002; XAVIBH.  
KW Hypotensive agent; Pyrrolidone carboxylic acid.  
FT MOD\_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.  
SQ SEQUENCE 11 AA; 1112 MW; 30BABF1277686777 CRC64;

Query Match 9.1%; Score 1; DB 1; Length 11;  
Best Local Similarity 100.0%; Pred. No. 9.8e+04;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 R 2  
|  
Db 3 R 3

# RESULT 20

CA21\_LITCI

ID CA21\_LITCI STANDARD; PRT; 11 AA.  
AC P82087;  
DT 16-OCT-2001 (Rel. 40, Created)  
DT 16-OCT-2001 (Rel. 40, Last sequence update)  
DT 10-OCT-2003 (Rel. 42, Last annotation update)  
DE Caerulein 2.1/2.1Y4.  
OS Litoria citropa (Australian blue mountains tree frog).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Amphibia; Batrachia; Anura; Neobatrachia; Hyloidea; Hylidae;  
OC Pelodyadinae; Litoria.  
OX NCBI\_TaxID=94770;  
RN [1]  
RP SEQUENCE, AND MASS SPECTROMETRY.  
RC TISSUE=Skin secretion;  
RX MEDLINE=20057701; PubMed=10589099;  
RA Wabnitz P.A., Bowie J.H., Tyler M.J.;  
RT "Caerulein-like peptides from the skin glands of the Australian blue  
RT mountains tree frog Litoria citropa. Part 1. Sequence determination  
RT using electrospray mass spectrometry."  
RL Rapid Commun. Mass Spectrom. 13:2498-2502(1999).  
CC -!- FUNCTION: Hypotensive neuropeptide (Probable).  
CC -!- SUBCELLULAR LOCATION: Secreted.  
CC -!- TISSUE SPECIFICITY: Skin dorsal glands.  
CC -!- PTM: Isoform 2.1Y4 differs from isoform 2.1 in not being  
CC sulfated.  
CC -!- MASS SPECTROMETRY: MW=1372; METHOD=Electrospray.  
CC -!- SIMILARITY: Belongs to the gastrin/cholecystokinin family.  
DR InterPro; IPR001651; Gastrin.  
DR PROSITE; PS00259; GASTRIN; FALSE\_NEG.  
KW Amphibian defense peptide; Hypotensive agent; Amidation; Sulfation;  
KW Pyrrolidone carboxylic acid.  
FT MOD\_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.  
FT MOD\_RES 4 4 SULFATION.  
FT MOD\_RES 11 11 AMIDATION.  
SQ SEQUENCE 11 AA; 1312 MW; 10DAB7C4EDD861BB CRC64;

Query Match 9.1%; Score 1; DB 1; Length 11;  
Best Local Similarity 100.0%; Pred. No. 9.8e+04;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 D 6  
|  
Db 3 D 3

# RESULT 21

CA22\_LITCI

ID CA22\_LITCI STANDARD; PRT; 11 AA.  
AC P82088;  
DT 16-OCT-2001 (Rel. 40, Created)  
DT 16-OCT-2001 (Rel. 40, Last sequence update)  
DT 10-OCT-2003 (Rel. 42, Last annotation update)  
DE Caerulein 2.2/2.2Y4.  
OS Litoria citropa (Australian blue mountains tree frog).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Amphibia; Batrachia; Anura; Neobatrachia; Hyloidea; Hylidae;  
 OC Pelodryadinae; Litoria.  
 OX NCBI\_TaxID=94770;  
 RN [1]  
 RP SEQUENCE, AND MASS SPECTROMETRY.  
 RC TISSUE=Skin secretion;  
 RX MEDLINE=20057701; PubMed=10589099;  
 RA Wabnitz P.A., Bowie J.H., Tyler M.J.;  
 RT "Caerulein-like peptides from the skin glands of the Australian blue  
 RT montains tree frog Litoria citropa. Part 1. Sequence determination  
 RT using electrospray mass spectrometry."  
 RL Rapid Commun. Mass Spectrom. 13:2498-2502(1999).  
 CC -!- FUNCTION: Hypotensive neuropeptide (Probable).  
 CC -!- SUBCELLULAR LOCATION: Secreted.  
 CC -!- TISSUE SPECIFICITY: Skin dorsal glands.  
 CC -!- PTM: Isoform 2.2Y4 differs from isoform 2.2 in not being  
 CC sulfated.  
 CC -!- MASS SPECTROMETRY: MW=1388; METHOD=Electrospray.  
 CC -!- SIMILARITY: Belongs to the gastrin/cholecystokinin family.  
 DR InterPro; IPR001651; Gastrin.  
 DR PROSITE; PS00259; GASTRIN; FALSE\_NEG.  
 KW Amphibian defense peptide; Hypotensive agent; Amidation; Sulfation;  
 KW Pyrrolidone carboxylic acid.  
 FT MOD\_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.  
 FT MOD\_RES 4 4 SULFATION.  
 FT MOD\_RES 11 11 AMIDATION.  
 SQ SEQUENCE 11 AA; 1328 MW; 10DAB894EDD861BB CRC64;

Query Match 9.1%; Score 1; DB 1; Length 11;  
 Best Local Similarity 100.0%; Pred. No. 9.8e+04;  
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 D 6  
 |  
 Db 3 D 3

# RESULT 22

## CA31\_LITCI

ID CA31\_LITCI STANDARD; PRT; 11 AA.  
 AC P82089;  
 DT 16-OCT-2001 (Rel. 40, Created)  
 DT 16-OCT-2001 (Rel. 40, Last sequence update)  
 DT 10-OCT-2003 (Rel. 42, Last annotation update)  
 DE Caerulein 3.1/3.1Y4.  
 OS Litoria citropa (Australian blue mountains tree frog).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Amphibia; Batrachia; Anura; Neobatrachia; Hyloidea; Hylidae;  
 OC Pelodryadinae; Litoria.  
 OX NCBI\_TaxID=94770;  
 RN [1]  
 RP SEQUENCE, AND MASS SPECTROMETRY.  
 RC TISSUE=Skin secretion;  
 RX MEDLINE=20057701; PubMed=10589099;  
 RA Wabnitz P.A., Bowie J.H., Tyler M.J.;  
 RT "Caerulein-like peptides from the skin glands of the Australian blue  
 RT montains tree frog Litoria citropa. Part 1. Sequence determination



RT using electrospray mass spectrometry.";  
 RL Rapid Commun. Mass Spectrom. 13:2498-2502(1999).  
 CC -!- FUNCTION: Hypotensive neuropeptide (Probable).  
 CC -!- SUBCELLULAR LOCATION: Secreted.  
 CC -!- TISSUE SPECIFICITY: Skin dorsal glands.  
 CC -!- PTM: Isoform 3.1Y4 differs from isoform 3.1 in not being  
 CC sulfated.  
 CC -!- MASS SPECTROMETRY: MW=1407; METHOD=Electrospray.  
 CC -!- SIMILARITY: Belongs to the gastrin/cholecystokinin family.  
 DR InterPro; IPR001651; Gastrin.  
 DR PROSITE; PS00259; GASTRIN; FALSE\_NEG.  
 KW Amphibian defense peptide; Hypotensive agent; Amidation; Sulfation;  
 KW Pyrrolidone carboxylic acid.  
 FT MOD\_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.  
 FT MOD\_RES 4 4 SULFATION.  
 FT MOD\_RES 11 11 AMIDATION.  
 SQ SEQUENCE 11 AA; 1347 MW; 10DAB7D67861A86B CRC64;

Query Match 9.1%; Score 1; DB 1; Length 11;  
 Best Local Similarity 100.0%; Pred. No. 9.8e+04;  
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 D 6  
 |  
 Db 3 D 3

# RESULT 23

CA32\_LITCI

ID CA32\_LITCI STANDARD; PRT; 11 AA.  
 AC P82090;  
 DT 16-OCT-2001 (Rel. 40, Created)  
 DT 16-OCT-2001 (Rel. 40, Last sequence update)  
 DT 10-OCT-2003 (Rel. 42, Last annotation update)  
 DE Caerulein 3.2/3.2Y4.  
 OS Litoria citropa (Australian blue mountains tree frog).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Amphibia; Batrachia; Anura; Neobatrachia; Hyloidea; Hylidae;  
 OC Pelodryadinae; Litoria.  
 OX NCBI\_TaxID=94770;  
 RN [1]  
 RP SEQUENCE, AND MASS SPECTROMETRY.  
 RC TISSUE=Skin secretion;  
 RX MEDLINE=20057701; PubMed=10589099;  
 RA Wabnitz P.A., Bowie J.H., Tyler M.J.;  
 RT "Caerulein-like peptides from the skin glands of the Australian blue  
 RT mountains tree frog Litoria citropa. Part 1. Sequence determination  
 RT using electrospray mass spectrometry.";  
 RL Rapid Commun. Mass Spectrom. 13:2498-2502(1999).  
 CC -!- FUNCTION: Hypotensive neuropeptide (Probable).  
 CC -!- SUBCELLULAR LOCATION: Secreted.  
 CC -!- TISSUE SPECIFICITY: Skin dorsal glands.  
 CC -!- PTM: Isoform 3.2Y4 differs from isoform 3.2 in not being  
 CC sulfated.  
 CC -!- MASS SPECTROMETRY: MW=1423; METHOD=Electrospray.  
 CC -!- SIMILARITY: Belongs to the gastrin/cholecystokinin family.  
 DR InterPro; IPR001651; Gastrin.

DR PROSITE; PS00259; GASTRIN; FALSE\_NEG.  
 KW Amphibian defense peptide; Hypotensive agent; Amidation; Sulfation;  
 KW Pyrrolidone carboxylic acid.  
 FT MOD\_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.  
 FT MOD\_RES 4 4 SULFATION.  
 FT MOD\_RES 11 11 AMIDATION.  
 SQ SEQUENCE 11 AA; 1363 MW; 10DAB8867861A86B CRC64;

Query Match 9.1%; Score 1; DB 1; Length 11;  
 Best Local Similarity 100.0%; Pred. No. 9.8e+04;  
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 D 6  
 |  
 Db 3 D 3

# RESULT 24

CA41\_LITCI  
 ID CA41\_LITCI STANDARD; PRT; 11 AA.  
 AC P82091;  
 DT 16-OCT-2001 (Rel. 40, Created)  
 DT 16-OCT-2001 (Rel. 40, Last sequence update)  
 DT 10-OCT-2003 (Rel. 42, Last annotation update)  
 DE Caerulein 4.1/4.1Y4.  
 OS Litoria citropa (Australian blue mountains tree frog).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Amphibia; Batrachia; Anura; Neobatrachia; Hyloidea; Hylidae;  
 OC Pelodyadinae; Litoria.  
 OX NCBI\_TaxID=94770;  
 RN [1]  
 RP SEQUENCE, AND MASS SPECTROMETRY.  
 RC TISSUE=Skin secretion;  
 RX MEDLINE=20057701; PubMed=10589099;  
 RA Wabnitz P.A., Bowie J.H., Tyler M.J.;  
 RT "Caerulein-like peptides from the skin glands of the Australian blue  
 RT mountains tree frog Litoria citropa. Part 1. Sequence determination  
 RT using electrospray mass spectrometry."  
 RL Rapid Commun. Mass Spectrom. 13:2498-2502(1999).  
 CC -!- FUNCTION: Hypotensive neuropeptide (Probable).  
 CC -!- SUBCELLULAR LOCATION: Secreted.  
 CC -!- TISSUE SPECIFICITY: Skin dorsal glands.  
 CC -!- PTM: Isoform 4.1Y4 differs from isoform 4.1 in not being  
 CC sulfated.  
 CC -!- MASS SPECTROMETRY: MW=1388; METHOD=Electrospray.  
 CC -!- SIMILARITY: Belongs to the gastrin/cholecystokinin family.  
 DR InterPro; IPR001651; Gastrin.  
 DR PROSITE; PS00259; GASTRIN; FALSE\_NEG.  
 KW Amphibian defense peptide; Hypotensive agent; Amidation; Sulfation;  
 KW Pyrrolidone carboxylic acid.  
 FT MOD\_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.  
 FT MOD\_RES 4 4 SULFATION.  
 FT MOD\_RES 11 11 AMIDATION.  
 SQ SEQUENCE 11 AA; 1328 MW; 10DAB7C4F5B861BB CRC64;

Query Match 9.1%; Score 1; DB 1; Length 11;  
 Best Local Similarity 100.0%; Pred. No. 9.8e+04;

Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 D 6  
|  
Db 3 D 3

RESULT 25

CA42\_LITCI

ID CA42\_LITCI STANDARD; PRT; 11 AA.  
AC P82092;  
DT 16-OCT-2001 (Rel. 40, Created)  
DT 16-OCT-2001 (Rel. 40, Last sequence update)  
DT 10-OCT-2003 (Rel. 42, Last annotation update)  
DE Caerulein 4.2/4.2Y4.  
OS Litoria citropa (Australian blue mountains tree frog).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Amphibia; Batrachia; Anura; Neobatrachia; Hyloidea; Hylidae;  
OC Pelodyadinae; Litoria.  
OX NCBI\_TaxID=94770;  
RN [1]  
RP SEQUENCE, AND MASS SPECTROMETRY.  
RC TISSUE=Skin secretion;  
RX MEDLINE=20057701; PubMed=10589099;  
RA Wabnitz P.A., Bowie J.H., Tyler M.J.;  
RT "Caerulein-like peptides from the skin glands of the Australian blue  
RT montains tree frog Litoria citropa. Part 1. Sequence determination  
RT using electrospray mass spectrometry."  
RL Rapid Commun. Mass Spectrom. 13:2498-2502(1999).  
CC -!- FUNCTION: Hypotensive neuropeptide (Probable).  
CC -!- SUBCELLULAR LOCATION: Secreted.  
CC -!- TISSUE SPECIFICITY: Skin dorsal glands.  
CC -!- PTM: Isoform 4.2Y4 differs from isoform 4.2 in not being  
CC sulfated.  
CC -!- MASS SPECTROMETRY: MW=1404; METHOD=Electrospray.  
CC -!- SIMILARITY: Belongs to the gastrin/cholecystokinin family.  
DR InterPro; IPR001651; Gastrin.  
DR PROSITE; PS00259; GASTRIN; FALSE\_NEG.  
KW Amphibian defense peptide; Hypotensive agent; Amidation; Sulfation;  
KW Pyrrolidone carboxylic acid.  
FT MOD\_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.  
FT MOD\_RES 4 4 SULFATION.  
FT MOD\_RES 11 11 AMIDATION.  
SQ SEQUENCE 11 AA; 1344 MW; 10DAB894F5B861BB CRC64;

Query Match 9.1%; Score 1; DB 1; Length 11;  
Best Local Similarity 100.0%; Pred. No. 9.8e+04;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 D 6  
|  
Db 3 D 3

RESULT 26

CEP1\_ACHFU

ID CEP1\_ACHFU STANDARD; PRT; 11 AA.

AC P22790;  
 DT 01-AUG-1991 (Rel. 19, Created)  
 DT 01-AUG-1991 (Rel. 19, Last sequence update)  
 DT 01-DEC-1992 (Rel. 24, Last annotation update)  
 DE Cardio-excitatory peptide-1 (ACEP-1).  
 OS Achatina fulica (Giant African snail).  
 OC Eukaryota; Metazoa; Mollusca; Gastropoda; Pulmonata; Stylommatophora;  
 OC Sigmurethra; Achatinoidea; Achatinidae; Achatina.  
 OX NCBI\_TaxID=6530;  
 RN [1]  
 RP SEQUENCE.  
 RC STRAIN=Ferussac; TISSUE=Heart atrium;  
 RX MEDLINE=90211261; PubMed=2322251;  
 RA Fujimoto K., Ohta N., Yoshida M., Kubota I., Muneoka Y., Kobayashi M.;  
 RT "A novel cardio-excitatory peptide isolated from the atria of the  
 RT African giant snail, Achatina fulica."  
 RL Biochem. Biophys. Res. Commun. 167:777-783(1990).  
 CC -!- FUNCTION: Potentiates the beat of the ventricle, and has also  
 CC excitatory actions on the penis retractor muscle, the buccal  
 CC muscle and the identified neurons controlling the buccal muscle  
 CC movement of achatina.  
 CC -!- SIMILARITY: TO POSSIBLE PEPTIDE L5 FROM APLYSIA.  
 DR PIR; A34662; A34662.  
 KW Hormone; Amidation.  
 FT MOD\_RES 11 11 AMIDATION.  
 SQ SEQUENCE 11 AA; 1305 MW; 82D6D5B9C7741365 CRC64;

Query Match 9.1%; Score 1; DB 1; Length 11;  
 Best Local Similarity 100.0%; Pred. No. 9.8e+04;  
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 S 4  
 |  
 Db 1 S 1

#### RESULT 27

##### COXA\_CANFA

ID COXA\_CANFA STANDARD; PRT; 11 AA.  
 AC P99501;  
 DT 15-JUL-1998 (Rel. 36, Created)  
 DT 15-JUL-1998 (Rel. 36, Last sequence update)  
 DT 30-MAY-2000 (Rel. 39, Last annotation update)  
 DE Cytochrome c oxidase polypeptide Va (EC 1.9.3.1) (Fragment).  
 GN COX5A.  
 OS Canis familiaris (Dog).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.  
 OX NCBI\_TaxID=9615;  
 RN [1]  
 RP SEQUENCE.  
 RC TISSUE=Heart;  
 RX MEDLINE=98163340; PubMed=9504812;  
 RA Dunn M.J., Corbett J.M., Wheeler C.H.;  
 RT "HSC-2DPAGE and the two-dimensional gel electrophoresis database of  
 RT dog heart proteins."  
 RL Electrophoresis 18:2795-2802(1997).

CC -!- FUNCTION: This is the heme A-containing chain of cytochrome c  
 CC oxidase, the terminal oxidase in mitochondrial electron transport.  
 CC -!- CATALYTIC ACTIVITY: 4 ferrocycytochrome c + O(2) = 4 ferricytochrome  
 CC c + 2 H(2)O.  
 CC -!- SUBCELLULAR LOCATION: Mitochondrial inner membrane.  
 CC -!- SIMILARITY: Belongs to the cytochrome c oxidase Va family.  
 DR HSC-2DPAGE; P99501; DOG.  
 DR InterPro; IPR003204; Cyt\_c\_ox5A.  
 DR Pfam; PF02284; COX5A; 1.  
 KW Oxidoreductase; Heme; Mitochondrion; Inner membrane.  
 FT NON\_TER 11 11  
 SQ SEQUENCE 11 AA; 1274 MW; 910B35C5B1AB11F5 CRC64;

Query Match 9.1%; Score 1; DB 1; Length 11;  
 Best Local Similarity 100.0%; Pred. No. 9.8e+04;  
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 S 4  
 |  
 Db 1 S 1

# RESULT 28

## CX5A\_CONAL

ID CX5A\_CONAL STANDARD; PRT; 11 AA.  
 AC P58848;  
 DT 28-FEB-2003 (Rel. 41, Created)  
 DT 28-FEB-2003 (Rel. 41, Last sequence update)  
 DT 15-MAR-2004 (Rel. 43, Last annotation update)  
 DE Conotoxin au5a.  
 OS Conus aulicus (Court cone).  
 OC Eukaryota; Metazoa; Mollusca; Gastropoda; Orthogastropoda;  
 OC Apogastropoda; Caenogastropoda; Sorbeoconcha; Hypsogastropoda;  
 OC Neogastropoda; Conoidea; Conidae; Conus.  
 OX NCBI\_TaxID=89437;  
 RN [1]  
 RP SEQUENCE, SYNTHESIS, AND MASS SPECTROMETRY.  
 RC TISSUE=Venom;  
 RX MEDLINE=99452958; PubMed=10521453;  
 RA Walker C.S., Steel D., Jacobsen R.B., Lirazan M.B., Cruz L.J.,  
 RA Hooper D., Shetty R., DelaCruz R.C., Nielsen J.S., Zhou L.M.,  
 RA Bandyopadhyay P., Craig A.G., Olivera B.M.;  
 RT "The T-superfamily of conotoxins."  
 RL J. Biol. Chem. 274:30664-30671(1999).  
 RN [2]  
 RP ERRATUM.  
 RA Walker C.S., Steel D., Jacobsen R.B., Lirazan M.B., Cruz L.J.,  
 RA Hooper D., Shetty R., DelaCruz R.C., Nielsen J.S., Zhou L.M.,  
 RA Bandyopadhyay P., Craig A.G., Olivera B.M.;  
 RL J. Biol. Chem. 274:36030-36030(1999).  
 CC -!- FUNCTION: Causes dorsal fins drooping in fish. No effect is  
 CC observed when injected into mice.  
 CC -!- SUBCELLULAR LOCATION: Secreted.  
 CC -!- TISSUE SPECIFICITY: Expressed by the venom duct.  
 CC -!- MASS SPECTROMETRY: MW=1436.6; METHOD=LSIMS.  
 CC -!- SIMILARITY: Belongs to the conotoxin T-superfamily.  
 DR PIR; A59146; A59146.

KW Toxin.  
FT DISULFID 2 9  
FT DISULFID 3 10  
SQ SEQUENCE 11 AA; 1441 MW; 21A36775440059D7 CRC64;

Query Match 9.1%; Score 1; DB 1; Length 11;  
Best Local Similarity 100.0%; Pred. No. 9.8e+04;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 R 2  
|  
Db 7 R 7

#### RESULT 29

##### CX5B\_CONAL

ID CX5B\_CONAL STANDARD; PRT; 11 AA.  
AC P58849;  
DT 28-FEB-2003 (Rel. 41, Created)  
DT 28-FEB-2003 (Rel. 41, Last sequence update)  
DT 15-MAR-2004 (Rel. 43, Last annotation update)  
DE Conotoxin au5b.  
OS Conus aulicus (Court cone).  
OC Eukaryota; Metazoa; Mollusca; Gastropoda; Orthogastropoda;  
OC Apogastropoda; Caenogastropoda; Sorbeoconcha; Hypsogastropoda;  
OC Neogastropoda; Conoidea; Conidae; Conus.  
OX NCBI\_TaxID=89437;  
RN [1]  
RP SEQUENCE, AND MASS SPECTROMETRY.  
RC TISSUE=Venom;  
RX MEDLINE=99452958; PubMed=10521453;  
RA Walker C.S., Steel D., Jacobsen R.B., Lirazan M.B., Cruz L.J.,  
RA Hooper D., Shetty R., Delacruz R.C., Nielsen J.S., Zhou L.M.,  
RA Bandyopadhyay P., Craig A.G., Olivera B.M.;  
RT "The T-superfamily of conotoxins."  
RL J. Biol. Chem. 274:30664-30671(1999).  
RN [2]  
RP ERRATUM.  
RA Walker C.S., Steel D., Jacobsen R.B., Lirazan M.B., Cruz L.J.,  
RA Hooper D., Shetty R., Delacruz R.C., Nielsen J.S., Zhou L.M.,  
RA Bandyopadhyay P., Craig A.G., Olivera B.M.;  
RL J. Biol. Chem. 274:36030-36030(1999).  
CC -!- FUNCTION: Causes dorsal fins drooping in fish. No effect is  
CC observed when injected into mice (By similarity).  
CC -!- SUBCELLULAR LOCATION: Secreted.  
CC -!- TISSUE SPECIFICITY: Expressed by the venom duct.  
CC -!- MASS SPECTROMETRY: MW=1388.6; METHOD=LSIMS.  
CC -!- SIMILARITY: Belongs to the conotoxin T-superfamily.  
DR PIR; B59146; B59146.  
KW Toxin.  
FT DISULFID 2 9  
FT DISULFID 3 10  
SQ SEQUENCE 11 AA; 1393 MW; 21A36775440042D7 CRC64;

Query Match 9.1%; Score 1; DB 1; Length 11;  
Best Local Similarity 100.0%; Pred. No. 9.8e+04;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 R 2  
|  
Db 7 R 7

RESULT 30

CXL1\_CONMR

ID CXL1\_CONMR STANDARD; PRT; 11 AA.  
AC P58807;  
DT 28-FEB-2003 (Rel. 41, Created)  
DT 28-FEB-2003 (Rel. 41, Last sequence update)  
DT 28-FEB-2003 (Rel. 41, Last annotation update)  
DE Lambda-conotoxin CMrVIA.  
OS Conus marmoreus (Marble cone).  
OC Eukaryota; Metazoa; Mollusca; Gastropoda; Orthogastropoda;  
OC Apogastropoda; Caenogastropoda; Sorbeoconcha; Hypsogastropoda;  
OC Neogastropoda; Conoidea; Conidae; Conus.  
OX NCBI\_TaxID=42752;  
RN [1]  
RP SEQUENCE, SYNTHESIS, AND MASS SPECTROMETRY.  
RC TISSUE=Venom;  
RX MEDLINE=20564325; PubMed=10988292;  
RA Balaji R.A., Ohtake A., Sato K., Gopalakrishnakone P., Kini R.M.,  
RA Seow K.T., Bay B.-H.;  
RT "Lambda-conotoxins, a new family of conotoxins with unique disulfide  
RT pattern and protein folding. Isolation and characterization from the  
RT venom of Conus marmoreus.";  
RL J. Biol. Chem. 275:39516-39522(2000).  
CC -!- FUNCTION: Inhibits the neuronal noradrenaline transporter.  
CC -!- SUBCELLULAR LOCATION: Secreted.  
CC -!- TISSUE SPECIFICITY: Expressed by the venom duct.  
CC -!- MASS SPECTROMETRY: MW=1237.93; MW\_ERR=0.21; METHOD=Electrospray.  
CC -!- SIMILARITY: Belongs to the chi/lambda-conotoxin family.  
KW Neurotoxin; Toxin; Hydroxylation.  
FT DISULFID 2 11  
FT DISULFID 3 8  
FT MOD\_RES 10 10 HYDROXYLATION.  
SQ SEQUENCE 11 AA; 1226 MW; 277AAC60B7232B58 CRC64;

Query Match 9.1%; Score 1; DB 1; Length 11;  
Best Local Similarity 100.0%; Pred. No. 9.8e+04;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 K 3  
|  
Db 6 K 6

RESULT 31

EFG\_CLOPA

ID EFG\_CLOPA STANDARD; PRT; 11 AA.  
AC P81350;  
DT 15-JUL-1998 (Rel. 36, Created)  
DT 15-JUL-1998 (Rel. 36, Last sequence update)  
DT 28-FEB-2003 (Rel. 41, Last annotation update)  
DE Elongation factor G (EF-G) (CP 5) (Fragment).

GN FUSA.  
 OS Clostridium pasteurianum.  
 OC Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;  
 OC Clostridium.  
 OX NCBI\_TaxID=1501;  
 RN [1]  
 RP SEQUENCE.  
 RC STRAIN=W5;  
 RX MEDLINE=98291870; PubMed=9629918;  
 RA Flengsrud R., Skjeldal L.;  
 RT "Two-dimensional gel electrophoresis separation and N-terminal  
 RT sequence analysis of proteins from Clostridium pasteurianum W5."  
 RL Electrophoresis 19:802-806(1998).  
 CC -!- FUNCTION: This protein promotes the GTP-dependent translocation of  
 CC the nascent protein chain from the A-site to the P-site of the  
 CC ribosome.  
 CC -!- SUBCELLULAR LOCATION: Cytoplasmic.  
 CC -!- SIMILARITY: Belongs to the GTP-binding elongation factor family.  
 CC EF-G/EF-2 subfamily.  
 DR InterPro; IPR000795; EF\_GTPbind.  
 DR PROSITE; PS00301; EFATOR\_GTP; PARTIAL.  
 KW Elongation factor; Protein biosynthesis; GTP-binding.  
 FT NON\_TER 11 11  
 SQ SEQUENCE 11 AA; 1337 MW; 412E71F1D9C33B17 CRC64;

Query Match 9.1%; Score 1; DB 1; Length 11;  
 Best Local Similarity 100.0%; Pred. No. 9.8e+04;  
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 K 3  
 |  
 Db 1 K 1

# RESULT 32

FAR6\_PENMO  
 ID FAR6\_PENMO STANDARD; PRT; 11 AA.  
 AC P83321;  
 DT 28-FEB-2003 (Rel. 41, Created)  
 DT 28-FEB-2003 (Rel. 41, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE FMRFamide-like neuropeptide FLP6 (DGRTPALRLRF-amide).  
 OS Penaeus monodon (Penaeid shrimp).  
 OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;  
 OC Eumalacostraca; Eucarida; Decapoda; Dendrobranchiata; Penaeoidea;  
 OC Penaeidae; Penaeus.  
 OX NCBI\_TaxID=6687;  
 RN [1]  
 RP SEQUENCE, AND MASS SPECTROMETRY.  
 RC TISSUE=Eyestalk;  
 RX MEDLINE=21956277; PubMed=11959015;  
 RA Sithigorngul P., Pupuem J., Krungkasem C., Longyant S.,  
 RA Chaivisuthangkura P., Sithigorngul W., Petsom A.;  
 RT "Seven novel FMRFamide-like neuropeptide sequences from the eyestalk  
 RT of the giant tiger prawn Penaeus monodon."  
 RL Comp. Biochem. Physiol. 131B:325-337(2002).  
 CC -!- SUBCELLULAR LOCATION: Secreted.



CC -!- MASS SPECTROMETRY: MW=1301.8; METHOD=MALDI.  
CC -!- SIMILARITY: Belongs to the FARP (FMRFamide related peptide)  
CC family.  
DR GO; GO:0007218; P:neuropeptide signaling pathway; TAS.  
KW Neuropeptide; Amidation.  
FT MOD\_RES 11 11 AMIDATION.  
SQ SEQUENCE 11 AA; 1301 MW; 9A19C860072DC771 CRC64;

Query Match 9.1%; Score 1; DB 1; Length 11;  
Best Local Similarity 100.0%; Pred. No. 9.8e+04;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 D 6  
|  
Db 1 D 1

#### RESULT 33

##### FAR9\_CALVO

ID FAR9\_CALVO STANDARD; PRT; 11 AA.  
AC P41864;  
DT 01-NOV-1995 (Rel. 32, Created)  
DT 01-NOV-1995 (Rel. 32, Last sequence update)  
DT 01-NOV-1995 (Rel. 32, Last annotation update)  
DE CalliFMRFamide 9.  
OS Calliphora vomitoria (Blue blowfly).  
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Oestroidea;  
OC Calliphoridae; Calliphora.  
OX NCBI\_TaxID=27454;  
RN [1]  
RP SEQUENCE.  
RC TISSUE=Thoracic ganglion;  
RX MEDLINE=92196111; PubMed=1549595;  
RA Duve H., Johnsen A.H., Sewell J.C., Scott A.G., Orchard I.,  
RA Rehfeld J.F., Thorpe A.;  
RT "Isolation, structure, and activity of -Phe-Met-Arg-Phe-NH2  
RT neuropeptides (designated calliFMRFamides) from the blowfly  
RT Calliphora vomitoria.";  
RL Proc. Natl. Acad. Sci. U.S.A. 89:2326-2330(1992).  
CC -!- SIMILARITY: Belongs to the FARP (FMRFamide related peptide)  
CC family.  
DR PIR; I41978; I41978.  
KW Neuropeptide; Amidation.  
FT MOD\_RES 11 11 AMIDATION.  
SQ SEQUENCE 11 AA; 1359 MW; 8160CE46CAA44321 CRC64;

Query Match 9.1%; Score 1; DB 1; Length 11;  
Best Local Similarity 100.0%; Pred. No. 9.8e+04;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 K 3  
|  
Db 5 K 5

#### RESULT 34

# HS70\_PINPS

ID HS70\_PINPS STANDARD; PRT; 11 AA.  
AC P81672;  
DT 15-JUL-1999 (Rel. 38, Created)  
DT 15-JUL-1999 (Rel. 38, Last sequence update)  
DT 15-MAR-2004 (Rel. 43, Last annotation update)  
DE Heat shock 70 kDa protein (Fragment).  
OS Pinus pinaster (Maritime pine).  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Coniferopsida; Coniferales; Pinaceae; Pinus.  
OX NCBI\_TaxID=71647;  
RN [1]  
RP SEQUENCE.  
RC TISSUE=Needle;  
RX MEDLINE=99274088; PubMed=10344291;  
RA Costa P., Pionneau C., Bauw G., Dubos C., Bahrman N., Kremer A.,  
RA Frigerio J.-M., Plomion C.;  
RT "Separation and characterization of needle and xylem maritime pine  
RT proteins.";  
RL Electrophoresis 20:1098-1108(1999).  
CC -!- MISCELLANEOUS: On the 2D-gel the determined pI of this protein  
CC (spot N164) is: 5.4, its MW is: 73 kDa.  
CC -!- SIMILARITY: Belongs to the heat shock protein 70 family.  
KW ATP-binding; Heat shock; Multigene family.  
FT NON\_TER 1 1  
FT NON\_TER 11 11  
SQ SEQUENCE 11 AA; 1228 MW; 037C1BE8DAA44DD0 CRC64;

Query Match 9.1%; Score 1; DB 1; Length 11;  
Best Local Similarity 100.0%; Pred. No. 9.8e+04;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 10 I 10  
|  
Db 3 I 3

## RESULT 35

### LADD\_ONCMY

ID LADD\_ONCMY STANDARD; PRT; 11 AA.  
AC P81018;  
DT 01-NOV-1997 (Rel. 35, Created)  
DT 01-NOV-1997 (Rel. 35, Last sequence update)  
DT 15-DEC-1998 (Rel. 37, Last annotation update)  
DE Ladderlectin (Fragment).  
OS Oncorhynchus mykiss (Rainbow trout) (Salmo gairdneri).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;  
OC Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.  
OX NCBI\_TaxID=8022;  
RN [1]  
RP SEQUENCE.  
RC TISSUE=Blood;  
RX MEDLINE=97293418; PubMed=9149391;  
RA Jensen L.E., Thiel S., Petersen T.E., Jensenuis J.C.;  
RT "A rainbow trout lectin with multimeric structure.";  
RL Comp. Biochem. Physiol. 116B:385-390(1997).

CC -!- FUNCTION: Lectin that binds sepharose.  
 CC -!- COFACTOR: Calcium is essential for sepharose binding.  
 CC -!- SUBUNIT: Multimeric.  
 KW Lectin; Calcium.  
 FT NON\_TER 11 11  
 SQ SEQUENCE 11 AA; 1163 MW; 0B26227FF6D45404 CRC64;

Query Match 9.1%; Score 1; DB 1; Length 11;  
 Best Local Similarity 100.0%; Pred. No. 9.8e+04;  
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 A 1  
 |  
 Db 1 A 1

# RESULT 36

LPW\_THETH

ID LPW\_THETH STANDARD; PRT; 11 AA.  
 AC P05624;  
 DT 01-NOV-1988 (Rel. 09, Created)  
 DT 01-NOV-1988 (Rel. 09, Last sequence update)  
 DT 30-MAY-2000 (Rel. 39, Last annotation update)  
 DE Trp operon leader peptide.  
 GN TRPL.  
 OS Thermus thermophilus.  
 OC Bacteria; Deinococcus-Thermus; Deinococci; Thermales; Thermaceae;  
 OC Thermus.  
 OX NCBI\_TaxID=274;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=HB8 / ATCC 27634;  
 RX MEDLINE=89000781; PubMed=2844259;  
 RA Sato S., Nakada Y., Kanaya S., Tanaka T.;  
 RT "Molecular cloning and nucleotide sequence of Thermus thermophilus  
 RT HB8 trpE and trpG."  
 RL Biochim. Biophys. Acta 950:303-312(1988).  
 CC -!- FUNCTION: THIS PROTEIN IS INVOLVED IN CONTROL OF THE BIOSYNTHESIS  
 CC OF TRYPTOPHAN.

CC -----  
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 CC -----

DR EMBL; X07744; CAA30565.1; -.  
 KW Tryptophan biosynthesis; Leader peptide.  
 SQ SEQUENCE 11 AA; 1228 MW; 364B295A772DC5A7 CRC64;

Query Match 9.1%; Score 1; DB 1; Length 11;  
 Best Local Similarity 100.0%; Pred. No. 9.8e+04;  
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 M 7

Db

1 M 1

RESULT 37

LSK1\_LEUMA

ID LSK1\_LEUMA STANDARD; PRT; 11 AA.  
AC P04428;  
DT 13-AUG-1987 (Rel. 05, Created)  
DT 13-AUG-1987 (Rel. 05, Last sequence update)  
DT 15-MAR-2004 (Rel. 43, Last annotation update)  
DE Leucosulfakinin-I (LSK-I).  
OS Leucophaea maderae (Madeira cockroach).  
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
OC Neoptera; Orthopteroidea; Dictyoptera; Blattaria; Blaberoidea;  
OC Blaberidae; Leucophaea.  
OX NCBI\_TaxID=6988;  
RN [1]  
RP SEQUENCE.  
RX MEDLINE=86315858; PubMed=3749893;  
RA Nachman R.J., Holman G.M., Haddon W.F., Ling N.;  
RT "Leucosulfakinin, a sulfated insect neuropeptide with homology to  
RT gastrin and cholecystokinin.";  
RL Science 234:71-73(1986).  
CC -!- FUNCTION: Change the frequency and amplitude of contractions of  
CC the hindgut. Inhibits muscle contraction of hindgut.  
CC -!- SIMILARITY: Belongs to the gastrin/cholecystokinin family.  
DR PIR; A01622; GMROL.  
DR InterPro; IPR001651; Gastrin.  
DR PROSITE; PS00259; GASTRIN; 1.  
KW Hormone; Amidation; Sulfation.  
FT MOD\_RES 6 6 SULFATION.  
FT MOD\_RES 11 11 AMIDATION.  
SQ SEQUENCE 11 AA; 1459 MW; 7E4E0680E86B5AAB CRC64;

Query Match 9.1%; Score 1; DB 1; Length 11;  
Best Local Similarity 100.0%; Pred. No. 9.8e+04;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 D 6

|

Db 5 D 5

RESULT 38

LSKP\_PERAM

ID LSKP\_PERAM STANDARD; PRT; 11 AA.  
AC P36885;  
DT 01-JUN-1994 (Rel. 29, Created)  
DT 01-JUN-1994 (Rel. 29, Last sequence update)  
DT 01-FEB-1996 (Rel. 33, Last annotation update)  
DE Perisulfakinin (Pea-SK-I).  
OS Periplaneta americana (American cockroach).  
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
OC Neoptera; Orthopteroidea; Dictyoptera; Blattaria; Blattoidea;  
OC Blattidae; Periplaneta.  
OX NCBI\_TaxID=6978;

RN [1]  
 RP SEQUENCE.  
 RC TISSUE=Corpora cardiaca;  
 RX MEDLINE=90137190; PubMed=2615921;  
 RA Veenstra J.A.;  
 RT "Isolation and structure of two gastrin/CCK-like neuropeptides from  
 RT the American cockroach homologous to the leucosulfakinins.";  
 RL Neuropeptides 14:145-149(1989).  
 CC -!- FUNCTION: Stimulates hindgut contractions.  
 CC -!- SIMILARITY: Belongs to the gastrin/cholecystokinin family.  
 DR PIR; A60656; A60656.  
 DR InterPro; IPR001651; Gastrin.  
 DR PROSITE; PS00259; GASTRIN; 1.  
 KW Hormone; Amidation; Sulfation.  
 FT MOD\_RES 6 6 SULFATION.  
 FT MOD\_RES 11 11 AMIDATION.  
 SQ SEQUENCE 11 AA; 1445 MW; 8B4E0680E86B5AAA CRC64;

Query Match 9.1%; Score 1; DB 1; Length 11;  
 Best Local Similarity 100.0%; Pred. No. 9.8e+04;  
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 D 6  
 |  
 Db 4 D 4

#### RESULT 39

##### MHBI\_KLEPN

ID MHBI\_KLEPN STANDARD; PRT; 11 AA.  
 AC P80580;  
 DT 01-OCT-1996 (Rel. 34, Created)  
 DT 01-OCT-1996 (Rel. 34, Last sequence update)  
 DT 01-NOV-1997 (Rel. 35, Last annotation update)  
 DE Maleylpyruvate isomerase (EC 5.2.1.4) (Fragment).  
 GN MHBI.  
 OS Klebsiella pneumoniae.  
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;  
 OC Enterobacteriaceae; Klebsiella.  
 OX NCBI\_TaxID=573;  
 RN [1]  
 RP SEQUENCE.  
 RX MEDLINE=96349117; PubMed=8760924;  
 RA Robson N.D., Parrott S., Cooper R.A.;  
 RT "In vitro formation of a catabolic plasmid carrying Klebsiella  
 RT pneumoniae DNA that allows growth of Escherichia coli K-12 on 3-  
 RT hydroxybenzoate.";  
 RL Microbiology 142:2115-2120(1996).  
 CC -!- CATALYTIC ACTIVITY: 3-maleylpyruvate = 3-fumarylpyruvate.  
 KW Isomerase.  
 FT NON\_TER 11 11  
 SQ SEQUENCE 11 AA; 1387 MW; 1EE0E2DD49C9D5AB CRC64;

Query Match 9.1%; Score 1; DB 1; Length 11;  
 Best Local Similarity 100.0%; Pred. No. 9.8e+04;  
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 M 7  
|  
Db 1 M 1

RESULT 40

MLG\_THETS

ID MLG\_THETS STANDARD; PRT; 11 AA.  
AC P41989;  
DT 01-NOV-1995 (Rel. 32, Created)  
DT 01-NOV-1995 (Rel. 32, Last sequence update)  
DT 16-OCT-2001 (Rel. 40, Last annotation update)  
DE Melanotropin gamma (Gamma-melanocyte stimulating hormone) (Gamma-MSH).  
OS Theromyzon tessulatum (Leech).  
OC Eukaryota; Metazoa; Annelida; Clitellata; Hirudinida; Hirudinea;  
OC Rhynchobdellida; Glossiphoniidae; Theromyzon.  
OX NCBI\_TaxID=13286;  
RN [1]  
RP SEQUENCE.  
RC TISSUE=Brain;  
RX MEDLINE=94298944; PubMed=8026574;  
RA Salzet M., Wattez C., Bulet P., Malecha J.;  
RT "Isolation and structural characterization of a novel peptide related  
RT to gamma-melanocyte stimulating hormone from the brain of the leech  
RT Theromyzon tessulatum.";  
RL FEBS Lett. 348:102-106(1994).  
CC -!- SIMILARITY: Belongs to the POMC family.  
DR PIR; S45698; S45698.  
KW Hormone; Amidation.  
FT MOD\_RES 11 11 AMIDATION.  
SQ SEQUENCE 11 AA; 1486 MW; 2DB8FACE6409C1E8 CRC64;

Query Match 9.1%; Score 1; DB 1; Length 11;  
Best Local Similarity 100.0%; Pred. No. 9.8e+04;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 R 2  
|  
Db 7 R 7

RESULT 41

MORN\_HUMAN

ID MORN\_HUMAN STANDARD; PRT; 11 AA.  
AC P01163;  
DT 21-JUL-1986 (Rel. 01, Created)  
DT 21-JUL-1986 (Rel. 01, Last sequence update)  
DT 28-FEB-2003 (Rel. 41, Last annotation update)  
DE Morphogenetic neuropeptide (Head activator) (HA).  
OS Homo sapiens (Human),  
OS Rattus norvegicus (Rat),  
OS Bos taurus (Bovine),  
OS Anthopleura elegantissima (Sea anemone), and  
OS Hydra attenuata (Hydra) (Hydra vulgaris).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606, 10116, 9913, 6110, 6087;

RN [1]  
 RP SEQUENCE.  
 RC SPECIES=Human, Rat, and Bovine;  
 RX MEDLINE=82035850; PubMed=7290191;  
 RA Bodenmuller H., Schaller H.C.;  
 RT "Conserved amino acid sequence of a neuropeptide, the head activator,  
 RT from coelenterates to humans.";  
 RL Nature 293:579-580(1981).  
 RN [2]  
 RP SEQUENCE.  
 RC SPECIES=A.elegantissima, and H.attenuata;  
 RA Schaller H.C., Bodenmuller H.;  
 RT "Isolation and amino acid sequence of a morphogenetic peptide from  
 RT hydra.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 78:7000-7004(1981).  
 RN [3]  
 RP SYNTHESIS.  
 RX MEDLINE=82050803; PubMed=7297679;  
 RA Birr C., Zachmann B., Bodenmuller H., Schaller H.C.;  
 RT "Synthesis of a new neuropeptide, the head activator from hydra.";  
 RL FEBS Lett. 131:317-321(1981).  
 RN [4]  
 RP FUNCTION.  
 RX MEDLINE=90059923; PubMed=2583101;  
 RA Schaller H.C., Druffel-Augustin S., Dubel S.;  
 RT "Head activator acts as an autocrine growth factor for NH15-CA2 cells  
 RT in the G2/mitosis transition.";  
 RL EMBO J. 8:3311-3318(1989).  
 CC -!- FUNCTION: HA acts as an autocrine growth factor for neural cells  
 CC in the G2/mitosis transition.  
 CC -!- CAUTION: This peptide was first isolated from nerve cells of hydra  
 CC and was called head activator by the authors, because it induced  
 CC head-specific growth and differentiation in this animal. It has  
 CC been found in mammalian intestine and hypothalamus.  
 DR PIR; A01427; YHRT.  
 DR PIR; A93900; YHXAE.  
 DR PIR; B01427; YHHU.  
 DR PIR; B93900; YHJFHY.  
 DR PIR; C01427; YHBO.  
 DR GK; P01163; -.  
 KW Growth factor; Cell cycle; Mitosis; Pyrrolidone carboxylic acid.  
 FT MOD RES 1 1 PYRROLIDONE CARBOXYLIC ACID.  
 SQ SEQUENCE 11 AA; 1142 MW; 37927417C325B878 CRC64;

Query Match 9.1%; Score 1; DB 1; Length 11;  
 Best Local Similarity 100.0%; Pred. No. 9.8e+04;  
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 S 4  
 |  
 Db 6 S 6

RESULT 42  
 OAIF\_SARBU  
 ID OAIF\_SARBU STANDARD; PRT; 11 AA.  
 AC P83518;

DT 10-OCT-2003 (Rel. 42, Created)  
 DT 10-OCT-2003 (Rel. 42, Last sequence update)  
 DT 10-OCT-2003 (Rel. 42, Last annotation update)  
 DE Ovary-derived ACE interactive factor (Neb-ODAIF) [Contains: Neb-ODAIF(1-9); Neb-ODAIF(1-7)].  
 OS Sarcophaga bullata (Grey flesh fly) (Neobellieria bullata).  
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
 OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Oestroidea;  
 OC Sarcophagidae; Sarcophaga.  
 OX NCBI\_TaxID=7385;  
 RN [1]  
 RP SEQUENCE, SYNTHESIS, CHARACTERIZATION, AND MASS SPECTROMETRY.  
 RC TISSUE=Ovary;  
 RX MEDLINE=22272747; PubMed=12383874;  
 RA Vandingenen A., Hens K., Baggerman G., Macours N., Schoofs L.,  
 RA De Loof A., Huybrechts R.;  
 RT "Isolation and characterization of an angiotensin converting enzyme  
 RT substrate from vitellogenic ovaries of Neobellieria bullata.";  
 RL Peptides 23:1853-1863(2002).  
 CC -!- FUNCTION: Substrate for angiotensin converting enzyme (ACE) in  
 CC vitro.  
 CC -!- PTM: ACE hydrolyzes Neb-ODAIF by sequentially cleaving off two C-  
 CC terminal dipeptides.  
 CC -!- MASS SPECTROMETRY: MW=1312.7; METHOD=MALDI; RANGE=1-11.  
 CC -!- SIMILARITY: To the N-terminal part of insect vitellogenins.  
 FT PEPTIDE 1 11 NEB-ODAIF.  
 FT PEPTIDE 1 9 NEB-ODAIF(1-9).  
 FT PEPTIDE 1 7 NEB-ODAIF(1-7).  
 SQ SEQUENCE 11 AA; 1314 MW; 4E114BB566C5A763 CRC64;

Query Match 9.1%; Score 1; DB 1; Length 11;  
 Best Local Similarity 100.0%; Pred. No. 9.8e+04;  
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 K 3  
 |  
 Db 2 K 2

#### RESULT 43

PKC1\_CARMO

ID PKC1\_CARMO STANDARD; PRT; 11 AA.  
 AC P82684;  
 DT 16-OCT-2001 (Rel. 40, Created)  
 DT 16-OCT-2001 (Rel. 40, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE Pyrokinin-1 (Cam-PK-1) (FXPRL-Amide).  
 OS Carausius morosus (Indian stick insect).  
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
 OC Neoptera; Orthopteroidea; Phasmatodea; Euphasmida; Phasmatoidea;  
 OC Heteronemiidae; Carausius.  
 OX NCBI\_TaxID=7022;  
 RN [1]  
 RP SEQUENCE, FUNCTION, AND MASS SPECTROMETRY.  
 RC TISSUE=Corpora cardiaca;  
 RA Predel R., Kellner R., Gaede G.;  
 RT "Myotropic neuropeptides from the retrocerebral complex of the stick



RT insect, *Carausius morosus* (Phasmatodea: Lonchodidae).";  
 RL Eur. J. Entomol. 96:275-278(1999).  
 CC -!- FUNCTION: Mediates visceral muscle contractile activity (myotropic  
 CC activity).  
 CC -!- MASS SPECTROMETRY: MW=1235; METHOD=MALDI.  
 CC -!- SIMILARITY: Belongs to the pyrokinin family.  
 DR InterPro; IPR001484; Pyrokinin.  
 DR PROSITE; PS00539; PYROKININ; FALSE\_NEG.  
 KW Neuropeptide; Amidation; Pyrokinin.  
 FT MOD\_RES 11 11 AMIDATION.  
 SQ SEQUENCE 11 AA; 1236 MW; 2BFA5225BB46C1A8 CRC64;

Query Match 9.1%; Score 1; DB 1; Length 11;  
 Best Local Similarity 100.0%; Pred. No. 9.8e+04;  
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 D 6  
 |  
 Db 1 D 1

#### RESULT 44

##### PVK1\_PERAM

ID PVK1\_PERAM STANDARD; PRT; 11 AA.  
 AC P41837;  
 DT 01-NOV-1995 (Rel. 32, Created)  
 DT 01-NOV-1995 (Rel. 32, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE Periviscerokinin-1 (Pea-PVK-1).  
 OS *Periplaneta americana* (American cockroach).  
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
 OC Neoptera; Orthopteroidea; Dictyoptera; Blattaria; Blattoidea;  
 OC Blattidae; *Periplaneta*.  
 OX NCBI\_TaxID=6978;  
 RN [1]  
 RP SEQUENCE, AND SYNTHESIS.  
 RC TISSUE=Abdominal perisymphathetic organs;  
 RX MEDLINE=95232021; PubMed=7716075;  
 RA Predel R., Linde D., Rapus J., Vettermann S., Penzlin H.;  
 RT "Periviscerokinin (Pea-PVK): a novel myotropic neuropeptide from the  
 RT perisymphathetic organs of the American cockroach."  
 RL Peptides 16:61-66(1995).  
 CC -!- FUNCTION: MYOACTIVE PEPTIDE; HAS EXCITORY ACTIONS ON THE  
 CC HYPERNEURAL MUSCLE.  
 KW Neuropeptide; Amidation.  
 FT MOD\_RES 11 11 AMIDATION.  
 SQ SEQUENCE 11 AA; 1114 MW; 39DB5419D7605728 CRC64;

Query Match 9.1%; Score 1; DB 1; Length 11;  
 Best Local Similarity 100.0%; Pred. No. 9.8e+04;  
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 A 1  
 |  
 Db 2 A 2

RESULT 45

RANC\_RANPI

ID RANC\_RANPI STANDARD; PRT; 11 AA.  
 AC P08951;  
 DT 01-NOV-1988 (Rel. 09, Created)  
 DT 01-NOV-1988 (Rel. 09, Last sequence update)  
 DT 10-OCT-2003 (Rel. 42, Last annotation update)  
 DE Ranatensin-C.  
 OS Rana pipiens (Northern leopard frog).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Ranidae; Rana.  
 OX NCBI\_TaxID=8404;  
 RN [1]  
 RP SEQUENCE.  
 RC TISSUE=Skin secretion;  
 RX MEDLINE=84131098; PubMed=6141890;  
 RA Nakajima T.;  
 RL Unpublished results, cited by:  
 RL Erspamer V., Erspamer G.F., Mazzanti G., Endean R.;  
 RL Comp. Biochem. Physiol. 77C:99-108(1984).  
 CC -!- SUBCELLULAR LOCATION: Secreted.  
 CC -!- TISSUE SPECIFICITY: Skin.  
 CC -!- SIMILARITY: Belongs to the bombesin/neuromedin B/ranatensin  
 CC family.  
 DR InterPro; IPR000874; Bombesin.  
 DR Pfam; PF02044; Bombesin; 1.  
 DR PROSITE; PS00257; BOMBESIN; 1.  
 KW Amphibian defense peptide; Bombesin family; Amidation.  
 FT MOD\_RES 11 11 AMIDATION.  
 SQ SEQUENCE 11 AA; 1304 MW; D6C9885A61ADC366 CRC64;

Query Match 9.1%; Score 1; DB 1; Length 11;  
 Best Local Similarity 100.0%; Pred. No. 9.8e+04;  
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 T 8  
 |  
 Db 2 T 2

RESULT 46

RE41\_LITRU

ID RE41\_LITRU STANDARD; PRT; 11 AA.  
 AC P82074;  
 DT 28-FEB-2003 (Rel. 41, Created)  
 DT 28-FEB-2003 (Rel. 41, Last sequence update)  
 DT 10-OCT-2003 (Rel. 42, Last annotation update)  
 DE Rubellidin 4.1.  
 OS Litoria rubella (Desert tree frog).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Amphibia; Batrachia; Anura; Neobatrachia; Hyloidea; Hylidae;  
 OC Pelodyadinae; Litoria.  
 OX NCBI\_TaxID=104895;  
 RN [1]  
 RP SEQUENCE, AND MASS SPECTROMETRY.  
 RC TISSUE=Skin secretion;  
 RA Steinborner S.T., Wabnitz P.A., Waugh R.J., Bowie J.H., Gao C.,

RA Tyler M.J., Wallace J.C.;  
 RT "The structure of new peptides from the Australin red tree frog  
 RT 'Litoria rubella'. The skin peptide profile as a probe for the study  
 RT of evolutionary trends of amphibians.";  
 RL Aust. J. Chem. 49:955-963(1996).  
 CC -!- FUNCTION: Shows neither neuropeptide activity nor antibiotic  
 CC activity.  
 CC -!- SUBCELLULAR LOCATION: Secreted.  
 CC -!- TISSUE SPECIFICITY: Expressed by the skin dorsal glands.  
 CC -!- MASS SPECTROMETRY: MW=1039; METHOD=FAB.  
 KW Amphibian defense peptide; Amidation.  
 FT MOD\_RES 11 11 AMIDATION.  
 SQ SEQUENCE 11 AA; 1040 MW; 84ED5CBC2877205A CRC64;

Query Match 9.1%; Score 1; DB 1; Length 11;  
 Best Local Similarity 100.0%; Pred. No. 9.8e+04;  
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 D 6  
 |  
 Db 4 D 4

# RESULT 47

## RRPL\_CHAV

ID RRPL\_CHAV STANDARD; PRT; 11 AA.  
 AC P13179;  
 DT 01-JAN-1990 (Rel. 13, Created)  
 DT 01-JAN-1990 (Rel. 13, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE RNA polymerase beta subunit (EC 2.7.7.48) (Large structural protein)  
 DE (L protein) (Fragment).  
 GN L.  
 OS Chandipura virus (strain I653514).  
 OC Viruses; ssRNA negative-strand viruses; Mononegavirales;  
 OC Rhabdoviridae; Vesiculovirus.  
 OX NCBI\_TaxID=11273;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=89299473; PubMed=2741347;  
 RA Masters P.S., Bhella R.S., Butcher M., Patel B., Ghosh H.P.,  
 RA Banerjee A.K.;  
 RT "Structure and expression of the glycoprotein gene of Chandipura  
 RT virus.";  
 RL Virology 171:285-290(1989).  
 CC -!- FUNCTION: THIS PROTEIN IS PROBABLY A COMPONENT OF THE ACTIVE  
 CC POLYMERASE. IT MAY FUNCTION IN RNA SYNTHESIS, CAPPING, AS WELL AS  
 CC METHYLATION OF CAPS, AND POLY(A) SYNTHESIS.  
 CC -!- CATALYTIC ACTIVITY: N nucleoside triphosphate = N diphosphate +  
 CC {RNA} (N).  
 CC -!- SUBUNIT: THOUGHT TO FORM A TRANSCRIPTION COMPLEX WITH THE  
 CC NUCLEOCAPSID (N) PROTEIN.  
 CC -!- SIMILARITY: WITH THE L PROTEIN OF OTHER RHABDOVIRUSES AND  
 CC PARAMYXOVIRUSES.  
 CC -----  
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CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
CC -----

DR EMBL; J04350; AAA42917.1; -.  
KW Transferase; RNA-directed RNA polymerase.  
FT NON\_TER 11 11  
SQ SEQUENCE 11 AA; 1189 MW; 0335D6E3AAB2D764 CRC64;

Query Match 9.1%; Score 1; DB 1; Length 11;  
Best Local Similarity 100.0%; Pred. No. 9.8e+04;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 M 7  
|  
Db 1 M 1

RESULT 48

T2P1\_PROVU

ID T2P1\_PROVU STANDARD; PRT; 11 AA.  
AC P31031;  
DT 01-JUL-1993 (Rel. 26, Created)  
DT 01-JUL-1993 (Rel. 26, Last sequence update)  
DT 10-OCT-2003 (Rel. 42, Last annotation update)  
DE Type II restriction enzyme PvuI (EC 3.1.21.4) (Endonuclease PvuI)  
DE (R.PvuI) (Fragment).  
GN PVUIR.  
OS *Proteus vulgaris*.  
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;  
OC Enterobacteriaceae; *Proteus*.  
OX NCBI\_TaxID=585;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=ATCC 13315;  
RX MEDLINE=93087186; PubMed=1454536;  
RA Smith M.D., Longo M., Gerard G.F., Chatterjee D.K.;  
RT "Cloning and characterization of genes for the PvuI restriction and  
RT modification system."  
RL Nucleic Acids Res. 20:5743-5747(1992).  
CC -!- FUNCTION: RECOGNIZES THE DOUBLE-STRANDED SEQUENCE CGATCG AND  
CC CLEAVES AFTER T-4.  
CC -!- CATALYTIC ACTIVITY: Endonucleolytic cleavage of DNA to give  
CC specific double-stranded fragments with terminal 5'-phosphates.  
CC -----

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CC -----

DR EMBL; L04163; AAA25660.1; -.  
DR PIR; S35490; S35490.

DR REBASE; 1541; PvuI.  
KW Restriction system; Hydrolase; Nuclease; Endonuclease.  
FT NON\_TER 1 1  
SQ SEQUENCE 11 AA; 1300 MW; 9F0CDE7955B72B1A CRC64;

Query Match 9.1%; Score 1; DB 1; Length 11;  
Best Local Similarity 100.0%; Pred. No. 9.8e+04;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 10 I 10  
|  
Db 1 I 1

#### RESULT 49

TIN1\_HOPTI  
ID TIN1\_HOPTI STANDARD; PRT; 11 AA.  
AC P82651;  
DT 16-OCT-2001 (Rel. 40, Created)  
DT 16-OCT-2001 (Rel. 40, Last sequence update)  
DT 15-MAR-2004 (Rel. 43, Last annotation update)  
DE Tigerinin-1.  
OS Hoplobatrachus tigerinus (Indian bull frog) (Rana tigerina).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Ranidae;  
OC Hoplobatrachus.  
OX NCBI\_TaxID=103373;  
RN [1]  
RP SEQUENCE, FUNCTION, MASS SPECTROMETRY, AND DISULFIDE BONDS.  
RC TISSUE=Skin secretion;  
RX PubMed=11031261;  
RA Purna Sai K., Jaganadham M.V., Vairamani M., Raju N.P.,  
RA Devi A.S., Nagaraj R., Sitaram N.;  
RT "Tigerinins: novel antimicrobial peptides from the Indian frog Rana  
RT tigerina.";  
RL J. Biol. Chem. 276:2701-2707(2001).  
CC -!- FUNCTION: Antibacterial activity against B.subtilis, E.coli,  
CC S.aureus, M.luteus, P.putida and S.cerevisiae.  
CC -!- SUBCELLULAR LOCATION: Secreted.  
CC -!- TISSUE SPECIFICITY: Skin.  
CC -!- MASS SPECTROMETRY: MW=1342; METHOD=MALDI.  
KW Amphibian defense peptide; Antibiotic; Fungicide; Amidation.  
FT DISULFID 2 10  
FT MOD\_RES 11 11 AMIDATION.  
SQ SEQUENCE 11 AA; 1344 MW; A2087DC960476056 CRC64;

Query Match 9.1%; Score 1; DB 1; Length 11;  
Best Local Similarity 100.0%; Pred. No. 9.8e+04;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 R 2  
|  
Db 9 R 9

#### RESULT 50

TKC2\_CALVO

ID TKC2\_CALVO STANDARD; PRT; 11 AA.  
AC P41518;  
DT 01-NOV-1995 (Rel. 32, Created)  
DT 01-NOV-1995 (Rel. 32, Last sequence update)  
DT 10-OCT-2003 (Rel. 42, Last annotation update)  
DE Callitachykinin II.  
OS Calliphora vomitoria (Blue blowfly).  
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Oestroidea;  
OC Calliphoridae; Calliphora.  
OX NCBI\_TaxID=27454;  
RN [1]  
RP SEQUENCE, AND SYNTHESIS.  
RX MEDLINE=95075727; PubMed=7984492;  
RA Lundquist C.T., Clottens F.L., Holman G.M., Nichols R., Nachman R.J.,  
RA Naessel D.R.;  
RT "Callitachykinin I and II, two novel myotropic peptides isolated from  
RT the blowfly, Calliphora vomitoria, that have resemblances to  
RT tachykinins.";  
RL Peptides 15:761-768(1994).  
CC -!- FUNCTION: Myoactive peptide.  
CC -!- SUBCELLULAR LOCATION: Secreted.  
CC -!- SIMILARITY: SOME SIMILARITY TO TACHYKININS.  
KW Tachykinin; Neuropeptide; Amidation.  
FT MOD\_RES 11 11 AMIDATION.  
SQ SEQUENCE 11 AA; 1103 MW; 15D7E3F9C9CDD444 CRC64;

Query Match 9.1%; Score 1; DB 1; Length 11;  
Best Local Similarity 100.0%; Pred. No. 9.8e+04;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 A 1  
|  
Db 6 A 6

# RESULT 51

## TKN1\_PSEGU

ID TKN1\_PSEGU STANDARD; PRT; 11 AA.  
AC P42986;  
DT 01-NOV-1995 (Rel. 32, Created)  
DT 01-NOV-1995 (Rel. 32, Last sequence update)  
DT 10-OCT-2003 (Rel. 42, Last annotation update)  
DE Kassinin-like peptide K-I (PG-KI).  
OS Pseudophryne guentheri (Guenther's toadlet).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Amphibia; Batrachia; Anura; Neobatrachia; Hyloidea; Myobatrachidae;  
OC Myobatrachinae; Pseudophryne.  
OX NCBI\_TaxID=30349;  
RN [1]  
RP SEQUENCE.  
RC TISSUE=Skin secretion;  
RX MEDLINE=90287814; PubMed=2356157;  
RA Simmaco M., Severini C., de Biase D., Barra D., Bossa F.,  
RA Roberts J.D., Melchiorri P., Erspamer V.;  
RT "Six novel tachykinin- and bombesin-related peptides from the skin of  
RT the Australian frog Pseudophryne guentheri.";

RL Peptides 11:299-304(1990).  
 CC -!- FUNCTION: Tachykinins are active peptides which excite neurons,  
 CC evoke behavioral responses, are potent vasodilators and  
 CC secretagogues, and contract (directly or indirectly) many smooth  
 CC muscles.  
 CC -!- SUBCELLULAR LOCATION: Secreted.  
 CC -!- TISSUE SPECIFICITY: Skin.  
 CC -!- SIMILARITY: Belongs to the tachykinin family.  
 DR PIR; B60409; B60409.  
 DR InterPro; IPR002040; Tachy\_Neurokinin.  
 DR InterPro; IPR008215; Tachykinin.  
 DR Pfam; PF02202; Tachykinin; 1.  
 DR SMART; SM00203; TK; 1.  
 DR PROSITE; PS00267; TACHYKININ; 1.  
 KW Amphibian defense peptide; Tachykinin; Neuropeptide; Amidation;  
 KW Pyrrolidone carboxylic acid.  
 FT MOD\_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.  
 FT MOD\_RES 11 11 AMIDATION.  
 SQ SEQUENCE 11 AA; 1269 MW; 3DBA7C37C9CB1AB7 CRC64;

Query Match 9.1%; Score 1; DB 1; Length 11;  
 Best Local Similarity 100.0%; Pred. No. 9.8e+04;  
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 D 6  
 |  
 Db 5 D 5

# RESULT 52

TKN1\_UPEIN  
 ID TKN1\_UPEIN STANDARD; PRT; 11 AA.  
 AC P82026;  
 DT 30-MAY-2000 (Rel. 39, Created)  
 DT 30-MAY-2000 (Rel. 39, Last sequence update)  
 DT 10-OCT-2003 (Rel. 42, Last annotation update)  
 DE Uperin 1.1.  
 OS Uperoleia inundata (Floodplain toadlet).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Amphibia; Batrachia; Anura; Neobatrachia; Hyloidea; Myobatrachidae;  
 OC Myobatrachinae; Uperoleia.  
 OX NCBI\_TaxID=104953;  
 RN [1]  
 RP SEQUENCE, AND MASS SPECTROMETRY.  
 RC TISSUE=Skin secretion;  
 RA Bradford A.M., Raftery M.J., Bowie J.H., Tyler M.J., Wallace J.C.,  
 RA Adams G.W., Severini C.;  
 RT "Novel uperin peptides from the dorsal glands of the australian  
 RT floodplain toadlet Uperoleia inundata."  
 RL Aust. J. Chem. 49:475-484(1996).  
 CC -!- FUNCTION: Tachykinins are active peptides which excite neurons,  
 CC evoke behavioral responses, are potent vasodilators and  
 CC secretagogues, and contract (directly or indirectly) many smooth  
 CC muscles.  
 CC -!- SUBCELLULAR LOCATION: Secreted.  
 CC -!- TISSUE SPECIFICITY: Skin dorsal glands.  
 CC -!- MASS SPECTROMETRY: MW=1208; METHOD=FAB.

CC -!- SIMILARITY: Belongs to the tachykinin family.  
 DR InterPro; IPR002040; Tachy\_Neurokinin.  
 DR Pfam; PF02202; Tachykinin; 1.  
 DR PROSITE; PS00267; TACHYKININ; 1.  
 KW Amphibian defense peptide; Tachykinin; Neuropeptide; Amidation;  
 KW Pyrrolidone carboxylic acid.  
 FT MOD\_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.  
 FT MOD\_RES 11 11 AMIDATION.  
 SQ SEQUENCE 11 AA; 1226 MW; 3293693E59CDD457 CRC64;

Query Match 9.1%; Score 1; DB 1; Length 11;  
 Best Local Similarity 100.0%; Pred. No. 9.8e+04;  
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 A 1  
 |  
 Db 2 A 2

# RESULT 53

TKN1\_UPERU  
 ID TKN1\_UPERU STANDARD; PRT; 11 AA.  
 AC P08612;  
 DT 01-AUG-1988 (Rel. 08, Created)  
 DT 01-FEB-1994 (Rel. 28, Last sequence update)  
 DT 10-OCT-2003 (Rel. 42, Last annotation update)  
 DE Uperolein.  
 OS Uperoleia rugosa (Wrinkled toadlet).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Amphibia; Batrachia; Anura; Neobatrachia; Hyloidea; Myobatrachidae;  
 OC Myobatrachinae; Uperoleia.  
 OX NCBI\_TaxID=8368;  
 RN [1]  
 RP SEQUENCE.  
 RC TISSUE=Skin secretion;  
 RX MEDLINE=75131227; PubMed=1120493;  
 RA Anastasi A., Erspamer V., Endean R.;  
 RT "Structure of uperolein, a physalaemin-like endecapeptide occurring  
 RT in the skin of Uperoleia rugosa and Uperoleia marmorata.";  
 RL Experientia 31:394-395(1975).  
 CC -!- FUNCTION: Tachykinins are active peptides which excite neurons,  
 CC evoke behavioral responses, are potent vasodilators and  
 CC secretagogues, and contract (directly or indirectly) many smooth  
 CC muscles.  
 CC -!- SUBCELLULAR LOCATION: Secreted.  
 CC -!- TISSUE SPECIFICITY: Skin.  
 CC -!- SIMILARITY: Belongs to the tachykinin family.  
 DR InterPro; IPR002040; Tachy\_Neurokinin.  
 DR InterPro; IPR008215; Tachykinin.  
 DR Pfam; PF02202; Tachykinin; 1.  
 DR SMART; SM00203; TK; 1.  
 DR PROSITE; PS00267; TACHYKININ; 1.  
 KW Amphibian defense peptide; Tachykinin; Neuropeptide; Amidation;  
 KW Pyrrolidone carboxylic acid.  
 FT MOD\_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.  
 FT MOD\_RES 11 11 AMIDATION.  
 SQ SEQUENCE 11 AA; 1252 MW; 32867C3E59CDD457 CRC64;



Query Match 9.1%; Score 1; DB 1; Length 11;  
Best Local Similarity 100.0%; Pred. No. 9.8e+04;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 D 6  
|  
Db 3 D 3

RESULT 54

TKN2\_PSEGU

ID TKN2\_PSEGU STANDARD; PRT; 11 AA.  
AC P42987;  
DT 01-NOV-1995 (Rel. 32, Created)  
DT 01-NOV-1995 (Rel. 32, Last sequence update)  
DT 10-OCT-2003 (Rel. 42, Last annotation update)  
DE Kassinin-like peptide K-II (PG-KII).  
OS Pseudophryne guentheri (Guenther's toadlet).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Amphibia; Batrachia; Anura; Neobatrachia; Hyla; Myobatrachidae;  
OC Myobatrachinae; Pseudophryne.  
OX NCBI\_TaxID=30349;  
RN [1]  
RP SEQUENCE.  
RC TISSUE=Skin secretion;  
RX MEDLINE=90287814; PubMed=2356157;  
RA Simmaco M., Severini C., de Biase D., Barra D., Bossa F.,  
RA Roberts J.D., Melchiorri P., Erspamer V.;  
RT "Six novel tachykinin- and bombesin-related peptides from the skin of  
RT the Australian frog Pseudophryne guentheri.";  
RL Peptides 11:299-304(1990).  
CC -!- FUNCTION: Tachykinins are active peptides which excite neurons,  
CC evoke behavioral responses, are potent vasodilators and  
CC secretagogues, and contract (directly or indirectly) many smooth  
CC muscles.  
CC -!- SUBCELLULAR LOCATION: Secreted.  
CC -!- TISSUE SPECIFICITY: Skin.  
CC -!- SIMILARITY: Belongs to the tachykinin family.  
DR PIR; C60409; C60409.  
DR InterPro; IPR002040; Tachy\_Neurokinin.  
DR InterPro; IPR008215; Tachykinin.  
DR Pfam; PF02202; Tachykinin; 1.  
DR SMART; SM00203; TK; 1.  
DR PROSITE; PS00267; TACHYKININ; 1.  
KW Amphibian defense peptide; Tachykinin; Neuropeptide; Amidation;  
KW Pyrrolidone carboxylic acid.  
FT MOD\_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.  
FT MOD\_RES 11 11 AMIDATION.  
SQ SEQUENCE 11 AA; 1246 MW; 3A247C37C9CB1AB7 CRC64;

Query Match 9.1%; Score 1; DB 1; Length 11;  
Best Local Similarity 100.0%; Pred. No. 9.8e+04;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 D 6  
|

## RESULT 55

TKN2\_UPERU

ID TKN2\_UPERU STANDARD; PRT; 11 AA.  
 AC P08616;  
 DT 01-AUG-1988 (Rel. 08, Created)  
 DT 01-FEB-1994 (Rel. 28, Last sequence update)  
 DT 10-OCT-2003 (Rel. 42, Last annotation update)  
 DE Rugosauperolein II ([Lys5,Thr6]physalaemin).  
 OS Uperoleia rugosa (Wrinkled toadlet).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Amphibia; Batrachia; Anura; Neobatrachia; Hylaidea; Myobatrachidae;  
 OC Myobatrachinae; Uperoleia.  
 OX NCBI\_TaxID=8368;  
 RN [1]  
 RP SEQUENCE.  
 RC TISSUE=Skin secretion;  
 RX MEDLINE=80223080; PubMed=7389029;  
 RA Nakajima T., Yasuhara T., Erspamer V., Erspamer G.F., Negri L.;  
 RT "Physalaemin- and bombesin-like peptides in the skin of the  
 RT Australian leptodactylid frog Uperoleia rugosa.";  
 RL Chem. Pharm. Bull. 28:689-695(1980).  
 CC -!- FUNCTION: Tachykinins are active peptides which excite neurons,  
 CC evoke behavioral responses, are potent vasodilators and  
 CC secretagogues, and contract (directly or indirectly) many smooth  
 CC muscles.  
 CC -!- SUBCELLULAR LOCATION: Secreted.  
 CC -!- TISSUE SPECIFICITY: Skin.  
 CC -!- SIMILARITY: Belongs to the tachykinin family.  
 DR InterPro; IPR002040; Tachy\_Neurokinin.  
 DR Pfam; PF02202; Tachykinin; 1.  
 DR PROSITE; PS00267; TACHYKININ; 1.  
 KW Amphibian defense peptide; Tachykinin; Neuropeptide; Amidation;  
 KW Pyrrolidone carboxylic acid.  
 FT MOD\_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.  
 FT MOD\_RES 11 11 AMIDATION.  
 SQ SEQUENCE 11 AA; 1270 MW; 3293693E59D1A327 CRC64;

Query Match 9.1%; Score 1; DB 1; Length 11;  
 Best Local Similarity 100.0%; Pred. No. 9.8e+04;  
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 A 1  
 |  
 Db 2 A 2

## RESULT 56

TKN3\_PSEGU

ID TKN3\_PSEGU STANDARD; PRT; 11 AA.  
 AC P42988;  
 DT 01-NOV-1995 (Rel. 32, Created)  
 DT 01-NOV-1995 (Rel. 32, Last sequence update)  
 DT 10-OCT-2003 (Rel. 42, Last annotation update)  
 DE Kassinin-like peptide K-III (PG-KIII).

OS Pseudophryne guentheri (Guenther's toadlet).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Amphibia; Batrachia; Anura; Neobatrachia; Hyloidea; Myobatrachidae;  
 OC Myobatrachinae; Pseudophryne.  
 OX NCBI\_TaxID=30349;  
 RN [1]  
 RP SEQUENCE.  
 RC TISSUE=Skin secretion;  
 RX MEDLINE=90287814; PubMed=2356157;  
 RA Simmaco M., Severini C., de Biase D., Barra D., Bossa F.,  
 RA Roberts J.D., Melchiorri P., Erspamer V.;  
 RT "Six novel tachykinin- and bombesin-related peptides from the skin of  
 RT the Australian frog Pseudophryne guntheri.";  
 RL Peptides 11:299-304(1990).  
 CC -!- FUNCTION: Tachykinins are active peptides which excite neurons,  
 CC evoke behavioral responses, are potent vasodilators and  
 CC secretagogues, and contract (directly or indirectly) many smooth  
 CC muscles.  
 CC -!- SUBCELLULAR LOCATION: Secreted.  
 CC -!- TISSUE SPECIFICITY: Skin.  
 CC -!- SIMILARITY: Belongs to the tachykinin family.  
 DR PIR; D60409; D60409.  
 DR InterPro; IPR002040; Tachy\_Neurokinin.  
 DR InterPro; IPR008215; Tachykinin.  
 DR Pfam; PF02202; Tachykinin; 1.  
 DR SMART; SM00203; TK; 1.  
 DR PROSITE; PS00267; TACHYKININ; 1.  
 KW Amphibian defense peptide; Tachykinin; Neuropeptide; Amidation;  
 KW Pyrrolidone carboxylic acid.  
 FT MOD\_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.  
 FT MOD\_RES 11 11 AMIDATION.  
 SQ SEQUENCE 11 AA; 1268 MW; 3DBA7C37C9CB1457 CRC64;

Query Match 9.1%; Score 1; DB 1; Length 11;  
 Best Local Similarity 100.0%; Pred. No. 9.8e+04;  
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 M 7  
 |  
 Db 11 M 11

# RESULT 57

TKN4\_PSEGU  
 ID TKN4\_PSEGU STANDARD; PRT; 11 AA.  
 AC P42989;  
 DT 01-NOV-1995 (Rel. 32, Created)  
 DT 01-NOV-1995 (Rel. 32, Last sequence update)  
 DT 10-OCT-2003 (Rel. 42, Last annotation update)  
 DE Substance P-like peptide I (PG-SPI).  
 OS Pseudophryne guentheri (Guenther's toadlet).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Amphibia; Batrachia; Anura; Neobatrachia; Hyloidea; Myobatrachidae;  
 OC Myobatrachinae; Pseudophryne.  
 OX NCBI\_TaxID=30349;  
 RN [1]  
 RP SEQUENCE.

RC TISSUE=Skin secretion;  
 RX MEDLINE=90287814; PubMed=2356157;  
 RA Simmaco M., Severini C., de Biase D., Barra D., Bossa F.,  
 RA Roberts J.D., Melchiorri P., Erspamer V.;  
 RT "Six novel tachykinin- and bombesin-related peptides from the skin of  
 RT the Australian frog *Pseudophryne guntheri*.";  
 RL Peptides 11:299-304(1990).  
 CC -!- FUNCTION: Tachykinins are active peptides which excite neurons,  
 CC evoke behavioral responses, are potent vasodilators and  
 CC secretagogues, and contract (directly or indirectly) many smooth  
 CC muscles.  
 CC -!- SUBCELLULAR LOCATION: Secreted.  
 CC -!- TISSUE SPECIFICITY: Skin.  
 CC -!- SIMILARITY: Belongs to the tachykinin family.  
 DR PIR; E60409; E60409.  
 DR InterPro; IPR002040; Tachy\_Neurokinin.  
 DR InterPro; IPR008215; Tachykinin.  
 DR Pfam; PF02202; Tachykinin; 1.  
 DR SMART; SM00203; TK; 1.  
 DR PROSITE; PS00267; TACHYKININ; 1.  
 KW Amphibian defense peptide; Tachykinin; Neuropeptide; Amidation;  
 KW Pyrrolidone carboxylic acid.  
 FT MOD\_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.  
 FT MOD\_RES 11 11 AMIDATION.  
 SQ SEQUENCE 11 AA; 1294 MW; 3A247C2CC9CB1AB7 CRC64;

Query Match 9.1%; Score 1; DB 1; Length 11;  
 Best Local Similarity 100.0%; Pred. No. 9.8e+04;  
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 D 6  
 |  
 Db 5 D 5

# RESULT 58

## TKN5\_PSEGU

ID TKN5\_PSEGU STANDARD; PRT; 11 AA.  
 AC P42990;  
 DT 01-NOV-1995 (Rel. 32, Created)  
 DT 01-NOV-1995 (Rel. 32, Last sequence update)  
 DT 10-OCT-2003 (Rel. 42, Last annotation update)  
 DE Substance P-like peptide II (PG-SPII).  
 OS *Pseudophryne guentheri* (Guenther's toadlet).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Amphibia; Batrachia; Anura; Neobatrachia; Hyloidea; Myobatrachidae;  
 OC Myobatrachinae; *Pseudophryne*.  
 OX NCBI\_TaxID=30349;  
 RN [1]  
 RP SEQUENCE.  
 RC TISSUE=Skin secretion;  
 RX MEDLINE=90287814; PubMed=2356157;  
 RA Simmaco M., Severini C., de Biase D., Barra D., Bossa F.,  
 RA Roberts J.D., Melchiorri P., Erspamer V.;  
 RT "Six novel tachykinin- and bombesin-related peptides from the skin of  
 RT the Australian frog *Pseudophryne guntheri*.";  
 RL Peptides 11:299-304(1990).

CC -!- FUNCTION: Tachykinins are active peptides which excite neurons,  
 CC evoke behavioral responses, are potent vasodilators and  
 CC secretagogues, and contract (directly or indirectly) many smooth  
 CC muscles.  
 CC -!- SUBCELLULAR LOCATION: Secreted.  
 CC -!- TISSUE SPECIFICITY: Skin.  
 CC -!- SIMILARITY: Belongs to the tachykinin family.  
 DR PIR; F60409; F60409.  
 DR InterPro; IPR002040; Tachy\_Neurokinin.  
 DR InterPro; IPR008215; Tachykinin.  
 DR Pfam; PF02202; Tachykinin; 1.  
 DR SMART; SM00203; TK; 1.  
 DR PROSITE; PS00267; TACHYKININ; 1.  
 KW Amphibian defense peptide; Tachykinin; Neuropeptide; Amidation;  
 KW Pyrrolidone carboxylic acid.  
 FT MOD\_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.  
 FT MOD\_RES 11 11 AMIDATION.  
 SQ SEQUENCE 11 AA; 1293 MW; 3A247C2CC9CB1457 CRC64;

Query Match 9.1%; Score 1; DB 1; Length 11;  
 Best Local Similarity 100.0%; Pred. No. 9.8e+04;  
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 M 7  
 |  
 Db 11 M 11

#### RESULT 59

##### TKNA\_CHICK

ID TKNA\_CHICK STANDARD; PRT; 11 AA.  
 AC P19850;  
 DT 01-FEB-1991 (Rel. 17, Created)  
 DT 01-FEB-1991 (Rel. 17, Last sequence update)  
 DT 10-OCT-2003 (Rel. 42, Last annotation update)  
 DE Substance P.  
 OS Gallus gallus (Chicken).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;  
 OC Gallus.  
 OX NCBI\_TaxID=9031;  
 RN [1]  
 RP SEQUENCE.  
 RC TISSUE=Intestine;  
 RX MEDLINE=88204263; PubMed=2452461;  
 RA Conlon J.M., Katsoulis S., Schmidt W.E., Thim L.;  
 RT "[Arg3]substance P and neurokinin A from chicken small intestine."  
 RL Regul. Pept. 20:171-180(1988).  
 CC -!- FUNCTION: Tachykinins are active peptides which excite neurons,  
 CC evoke behavioral responses, are potent vasodilators and  
 CC secretagogues, and contract (directly or indirectly) many smooth  
 CC muscles.  
 CC -!- SUBCELLULAR LOCATION: Secreted.  
 CC -!- SIMILARITY: Belongs to the tachykinin family.  
 DR PIR; JN0023; JN0023.  
 DR InterPro; IPR002040; Tachy\_Neurokinin.  
 DR Pfam; PF02202; Tachykinin; 1.

DR PROSITE; PS00267; TACHYKININ; 1.  
KW Tachykinin; Neuropeptide; Amidation; Neurotransmitter.  
FT MOD\_RES 11 11 AMIDATION.  
SQ SEQUENCE 11 AA; 1377 MW; 21487FE3C9D6C6C7 CRC64;

Query Match 9.1%; Score 1; DB 1; Length 11;  
Best Local Similarity 100.0%; Pred. No. 9.8e+04;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 R 2  
|  
Db 1 R 1

#### RESULT 60

TKNA\_GADMO

ID TKNA\_GADMO STANDARD; PRT; 11 AA.  
AC P28498;  
DT 01-DEC-1992 (Rel. 24, Created)  
DT 01-DEC-1992 (Rel. 24, Last sequence update)  
DT 10-OCT-2003 (Rel. 42, Last annotation update)  
DE Substance P.  
OS Gadus morhua (Atlantic cod).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;  
OC Acanthomorpha; Paracanthopterygii; Gadiformes; Gadidae; Gadus.  
OX NCBI\_TaxID=8049;  
RN [1]  
RP SEQUENCE.  
RC TISSUE=Brain;  
RX MEDLINE=92298992; PubMed=1376687;  
RA Jensen J., Conlon J.M.;  
RT "Substance-P-related and neurokinin-A-related peptides from the brain  
RT of the cod and trout."  
RL Eur. J. Biochem. 206:659-664(1992).  
CC -!- FUNCTION: Tachykinins are active peptides which excite neurons,  
CC evoke behavioral responses, are potent vasodilators and  
CC secretagogues, and contract (directly or indirectly) many smooth  
CC muscles.  
CC -!- SUBCELLULAR LOCATION: Secreted.  
CC -!- SIMILARITY: Belongs to the tachykinin family.  
DR PIR; S23306; S23306.  
DR InterPro; IPR002040; Tachy\_Neurokinin.  
DR InterPro; IPR008215; Tachykinin.  
DR Pfam; PF02202; Tachykinin; 1.  
DR SMART; SM00203; TK; 1.  
DR PROSITE; PS00267; TACHYKININ; 1.  
KW Tachykinin; Neuropeptide; Amidation; Neurotransmitter.  
FT MOD\_RES 11 11 AMIDATION (BY SIMILARITY).  
SQ SEQUENCE 11 AA; 1315 MW; 214860D759D6C6C7 CRC64;

Query Match 9.1%; Score 1; DB 1; Length 11;  
Best Local Similarity 100.0%; Pred. No. 9.8e+04;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 K 3  
|

Db 1 K 1

RESULT 61

TKNA\_HORSE

ID TKNA\_HORSE STANDARD; PRT; 11 AA.  
AC P01290;  
DT 21-JUL-1986 (Rel. 01, Created)  
DT 21-JUL-1986 (Rel. 01, Last sequence update)  
DT 10-OCT-2003 (Rel. 42, Last annotation update).  
DE Substance P.  
GN TAC1 OR NKNA OR TAC2 OR NKA.  
OS Equus caballus (Horse), and  
OS Cavia porcellus (Guinea pig).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Perissodactyla; Equidae; Equus.  
OX NCBI\_TaxID=9796, 10141;  
RN [1]  
RP SEQUENCE.  
RC SPECIES=Horse;  
RA Studer R.O., Trzeciak A., Lergier W.;  
RT "Isolation and amino-acid sequence of substance P from horse  
RT intestine.";  
RL Helv. Chim. Acta 56:860-866(1973).  
RN [2]  
RP SEQUENCE.  
RC SPECIES=C.porcellus;  
RX MEDLINE=90044685; PubMed=2478925;  
RA Murphy R.;  
RT "Primary amino acid sequence of guinea-pig substance P.";  
RL Neuropeptides 14:105-110(1989).  
CC -!- FUNCTION: Tachykinins are active peptides which excite neurons,  
CC evoke behavioral responses, are potent vasodilators and  
CC secretagogues, and contract (directly or indirectly) many smooth  
CC muscles.  
CC -!- SUBCELLULAR LOCATION: Secreted.  
CC -!- SIMILARITY: Belongs to the tachykinin family.  
DR PIR; A01558; SPHO.  
DR PIR; A60654; A60654.  
DR InterPro; IPR002040; Tachy\_Neurokinin.  
DR InterPro; IPR008215; Tachykinin.  
DR Pfam; PF02202; Tachykinin; 1.  
DR SMART; SM00203; TK; 1.  
DR PROSITE; PS00267; TACHYKININ; 1.  
KW Tachykinin; Neuropeptide; Amidation; Neurotransmitter.  
FT MOD\_RES 11 11 AMIDATION.  
SQ SEQUENCE 11 AA; 1349 MW; 3E757FE3C9D6C6C7 CRC64;

Query Match 9.1%; Score 1; DB 1; Length 11;  
Best Local Similarity 100.0%; Pred. No. 9.8e+04;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 R 2  
|  
Db 1 R 1

## RESULT 62

TKNA\_ONCMY

ID TKNA\_ONCMY STANDARD; PRT; 11 AA.  
 AC P28499;  
 DT 01-DEC-1992 (Rel. 24, Created)  
 DT 01-DEC-1992 (Rel. 24, Last sequence update)  
 DT 10-OCT-2003 (Rel. 42, Last annotation update)  
 DE Substance P.  
 OS Oncorhynchus mykiss (Rainbow trout) (Salmo gairdneri).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;  
 OC Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.  
 OX NCBI\_TaxID=8022;  
 RN [1]  
 RP SEQUENCE.  
 RC TISSUE=Brain;  
 RX MEDLINE=92298992; PubMed=1376687;  
 RA Jensen J., Conlon J.M.;  
 RT "Substance-P-related and neurokinin-A-related peptides from the brain  
 RT of the cod and trout."  
 RL Eur. J. Biochem. 206:659-664(1992).  
 CC -!- FUNCTION: Tachykinins are active peptides which excite neurons,  
 CC evoke behavioral responses, are potent vasodilators and  
 CC secretagogues, and contract (directly or indirectly) many smooth  
 CC muscles.  
 CC -!- SUBCELLULAR LOCATION: Secreted.  
 CC -!- SIMILARITY: Belongs to the tachykinin family.  
 DR PIR; S23308; S23308.  
 DR InterPro; IPR002040; Tachy\_Neurokinin.  
 DR InterPro; IPR008215; Tachykinin.  
 DR Pfam; PF02202; Tachykinin; 1.  
 DR SMART; SM00203; TK; 1.  
 DR PROSITE; PS00267; TACHYKININ; 1.  
 KW Tachykinin; Neuropeptide; Amidation; Neurotransmitter.  
 FT MOD\_RES 11 11 AMIDATION (BY SIMILARITY).  
 SQ SEQUENCE 11 AA; 1358 MW; 214860DEC9D6D1F7 CRC64;

Query Match 9.1%; Score 1; DB 1; Length 11;  
 Best Local Similarity 100.0%; Pred. No. 9.8e+04;  
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 K 3  
 |  
 Db 1 K 1

## RESULT 63

TKNA\_RANCA

ID TKNA\_RANCA STANDARD; PRT; 11 AA.  
 AC P22688;  
 DT 01-AUG-1991 (Rel. 19, Created)  
 DT 01-AUG-1991 (Rel. 19, Last sequence update)  
 DT 10-OCT-2003 (Rel. 42, Last annotation update)  
 DE Ranatachykinin A (RTK A).  
 OS Rana catesbeiana (Bull frog).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Ranidae; Rana.



OX NCBI\_TaxID=8400;  
 RN [1]  
 RP SEQUENCE, AND SYNTHESIS.  
 RC TISSUE=Brain, and Intestine;  
 RX MEDLINE=91254337; PubMed=2043143;  
 RA Kozawa H., Hino J., Minamino N., Kangawa K., Matsuo H.;  
 RT "Isolation of four novel tachykinins from frog (*Rana catesbeiana*)  
 RT brain and intestine.";  
 RL Biochem. Biophys. Res. Commun. 177:588-595(1991).  
 RN [2]  
 RP SEQUENCE.  
 RC TISSUE=Intestine;  
 RX MEDLINE=94023216; PubMed=8210506;  
 RA Kangawa K., Kozawa H., Hino J., Minamino N., Matsuo H.;  
 RT "Four novel tachykinins in frog (*Rana catesbeiana*) brain and  
 RT intestine.";  
 RL Regul. Pept. 46:81-88(1993).  
 CC -!- FUNCTION: Tachykinins are active peptides which excite neurons,  
 CC evoke behavioral responses, are potent vasodilators and  
 CC secretagogues, and contract (directly or indirectly) many smooth  
 CC muscles.  
 CC -!- SUBCELLULAR LOCATION: Secreted.  
 CC -!- SIMILARITY: Belongs to the tachykinin family.  
 DR PIR; A61033; A61033.  
 DR InterPro; IPR002040; Tachy\_Neurokinin.  
 DR InterPro; IPR008215; Tachykinin.  
 DR Pfam; PF02202; Tachykinin; 1.  
 DR SMART; SM00203; TK; 1.  
 DR PROSITE; PS00267; TACHYKININ; 1.  
 KW Tachykinin; Neuropeptide; Amidation.  
 FT MOD\_RES 11 11 AMIDATION.  
 SQ SEQUENCE 11 AA; 1311 MW; 200D60CC59D40AB7 CRC64;

Query Match 9.1%; Score 1; DB 1; Length 11;  
 Best Local Similarity 100.0%; Pred. No. 9.8e+04;  
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 K 3  
 |  
 Db 1 K 1

# RESULT 64

TKNA\_RANRI  
 ID TKNA\_RANRI STANDARD; PRT; 11 AA.  
 AC P29207;  
 DT 01-DEC-1992 (Rel. 24, Created)  
 DT 01-DEC-1992 (Rel. 24, Last sequence update)  
 DT 10-OCT-2003 (Rel. 42, Last annotation update)  
 DE Ranakinin (Substance-P-related peptide).  
 OS *Rana ridibunda* (Laughing frog) (Marsh frog).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Ranidae; *Rana*.  
 OX NCBI\_TaxID=8406;  
 RN [1]  
 RP SEQUENCE.  
 RC TISSUE=Brain;

RX MEDLINE=92044543; PubMed=1658233;  
 RA O'Harte F., Burcher E., Lovas S., Smith D.D., Vaudry H., Conlon J.M.;  
 RT "Ranakinin: a novel NK1 tachykinin receptor agonist isolated with  
 RT neurokinin B from the brain of the frog *Rana ridibunda*.";  
 RL J. Neurochem. 57:2086-2091(1991).  
 CC -!- FUNCTION: Tachykinins are active peptides which excite neurons,  
 CC evoke behavioral responses, are potent vasodilators and  
 CC secretagogues, and contract (directly or indirectly) many smooth  
 CC muscles.  
 CC -!- SUBCELLULAR LOCATION: Secreted.  
 CC -!- SIMILARITY: Belongs to the tachykinin family.  
 DR InterPro; IPR002040; Tachy\_Neurokinin.  
 DR InterPro; IPR008215; Tachykinin.  
 DR Pfam; PF02202; Tachykinin; 1.  
 DR SMART; SM00203; TK; 1.  
 DR PROSITE; PS00267; TACHYKININ; 1.  
 KW Tachykinin; Neuropeptide; Amidation.  
 FT MOD\_RES 11 11 AMIDATION.  
 SQ SEQUENCE 11 AA; 1352 MW; 3A2460CC59D40B07 CRC64;

Query Match 9.1%; Score 1; DB 1; Length 11;  
 Best Local Similarity 100.0%; Pred. No. 9.8e+04;  
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 K 3  
 |  
 Db 1 K 1

#### RESULT 65

TKNA\_SCYCA

ID TKNA\_SCYCA STANDARD; PRT; 11 AA.  
 AC P41333;  
 DT 01-FEB-1995 (Rel. 31, Created)  
 DT 01-FEB-1995 (Rel. 31, Last sequence update)  
 DT 10-OCT-2003 (Rel. 42, Last annotation update)  
 DE Substance P.  
 OS *Scyliorhinus canicula* (Spotted dogfish) (Spotted catshark).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Chondrichthyes;  
 OC Elasmobranchii; Galeomorphii; Galeoidea; Carcharhiniformes;  
 OC Scyliorhinidae; *Scyliorhinus*.  
 OX NCBI\_TaxID=7830;  
 RN [1]  
 RP SEQUENCE.  
 RC TISSUE=Brain;  
 RX MEDLINE=93292508; PubMed=7685693;  
 RA Waugh D., Wang Y., Hazon N., Balment R.J., Conlon J.M.;  
 RT "Primary structures and biological activities of substance-P-related  
 RT peptides from the brain of the dogfish, *Scyliorhinus canicula*.";  
 RL Eur. J. Biochem. 214:469-474(1993).  
 CC -!- FUNCTION: Tachykinins are active peptides which excite neurons,  
 CC evoke behavioral responses, are potent vasodilators and  
 CC secretagogues, and contract (directly or indirectly) many smooth  
 CC muscles.  
 CC -!- SUBCELLULAR LOCATION: Secreted.  
 CC -!- SIMILARITY: Belongs to the tachykinin family.  
 DR PIR; S33300; S33300.

DR InterPro; IPR002040; Tachy Neurokinin.  
DR PROSITE; PS00267; TACHYKININ; 1.  
KW Tachykinin; Neuropeptide; Amidation; Neurotransmitter.  
FT MOD\_RES 11 11 AMIDATION.  
SQ SEQUENCE 11 AA; 1278 MW; 214860DEC9D6D867 CRC64;

Query Match 9.1%; Score 1; DB 1; Length 11;  
Best Local Similarity 100.0%; Pred. No. 9.8e+04;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 K 3  
|  
Db 1 K 1

#### RESULT 66

##### TKND\_RANCA

ID TKND\_RANCA STANDARD; PRT; 11 AA.  
AC P22691;  
DT 01-AUG-1991 (Rel. 19, Created)  
DT 01-AUG-1991 (Rel. 19, Last sequence update)  
DT 10-OCT-2003 (Rel. 42, Last annotation update)  
DE Ranatachykinin D (RTK D).  
OS Rana catesbeiana (Bull frog).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Ranidae; Rana.  
OX NCBI\_TaxID=8400;  
RN [1]  
RP SEQUENCE, AND SYNTHESIS.  
RC TISSUE=Intestine;  
RX MEDLINE=91254337; PubMed=2043143;  
RA Kozawa H., Hino J., Minamino N., Kangawa K., Matsuo H.;  
RT "Isolation of four novel tachykinins from frog (Rana catesbeiana)  
RT brain and intestine.";  
RL Biochem. Biophys. Res. Commun. 177:588-595(1991).  
RN [2]  
RP SEQUENCE.  
RC TISSUE=Intestine;  
RX MEDLINE=94023216; PubMed=8210506;  
RA Kangawa K., Kozawa H., Hino J., Minamino N., Matsuo H.;  
RT "Four novel tachykinins in frog (Rana catesbeiana) brain and  
RT intestine.";  
RL Regul. Pept. 46:81-88(1993).  
CC -!- FUNCTION: Tachykinins are active peptides which excite neurons,  
CC evoke behavioral responses, are potent vasodilators and  
CC secretagogues, and contract (directly or indirectly) many smooth  
CC muscles.  
CC -!- SUBCELLULAR LOCATION: Secreted.  
CC -!- SIMILARITY: Belongs to the tachykinin family.  
DR PIR; D61033; D61033.  
DR InterPro; IPR002040; Tachy Neurokinin.  
DR PROSITE; PS00267; TACHYKININ; FALSE\_NEG.  
KW Tachykinin; Neuropeptide; Amidation.  
FT MOD\_RES 11 11 AMIDATION.  
SQ SEQUENCE 11 AA; 1350 MW; 3A34256C59D40B07 CRC64;

Query Match 9.1%; Score 1; DB 1; Length 11;

Best Local Similarity 100.0%; Pred. No. 9.8e+04;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 K 3  
|  
Db 1 K 1

RESULT 67

TKN\_ELEMO

ID TKN\_ELEMO STANDARD; PRT; 11 AA.  
AC P01293;  
DT 21-JUL-1986 (Rel. 01, Created)  
DT 01-FEB-1994 (Rel. 28, Last sequence update)  
DT 10-OCT-2003 (Rel. 42, Last annotation update)  
DE Eledoisin.  
OS Eledone moschata (Musky octopus) (Ozaena moschata), and  
OS Eledone cirrhosa (Curled octopus) (Ozaena cirrosa).  
OC Eukaryota; Metazoa; Mollusca; Cephalopoda; Coleoidea; Neocoleoidea;  
OC Octopodiformes; Octopoda; Incirrata; Octopodidae; Eledone.  
OX NCBI\_TaxID=6641, 102876;  
RN [1]  
RP SEQUENCE.  
RA Anastasi A., Erspamer V.;  
RT "The isolation and amino acid sequence of eledoisin, the active  
RT endecapeptide of the posterior salivary glands of Eledone.";  
RL Arch. Biochem. Biophys. 101:56-65(1963).  
CC -!- FUNCTION: Tachykinins are active peptides which excite neurons,  
CC evoke behavioral responses, are potent vasodilators and  
CC secretagogues, and contract (directly or indirectly) many smooth  
CC muscles.  
CC -!- SUBCELLULAR LOCATION: Secreted.  
CC -!- TISSUE SPECIFICITY: Skin.  
CC -!- SIMILARITY: Belongs to the tachykinin family.  
DR PIR; A01561; EOOC.  
DR PIR; B01561; EOCC.  
DR PDB; 1MXQ; 18-FEB-03.  
DR InterPro; IPR002040; Tachy\_Neurokinin.  
DR PROSITE; PS00267; TACHYKININ; 1.  
KW Tachykinin; Neuropeptide; Amidation; Pyrrolidone carboxylic acid;  
KW 3D-structure.  
FT MOD\_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.  
FT MOD\_RES 11 11 AMIDATION.  
SQ SEQUENCE 11 AA; 1206 MW; 570D7C2559CDDAA3 CRC64;

Query Match 9.1%; Score 1; DB 1; Length 11;  
Best Local Similarity 100.0%; Pred. No. 9.8e+04;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 S 4  
|  
Db 3 S 3

RESULT 68

TKN\_PHYFU

ID TKN\_PHYFU STANDARD; PRT; 11 AA.

AC P08615;  
 DT 01-AUG-1988 (Rel. 08, Created)  
 DT 01-FEB-1994 (Rel. 28, Last sequence update)  
 DT 10-OCT-2003 (Rel. 42, Last annotation update)  
 DE Physalaemin.  
 OS Physalaemus fuscumaculatus (Neotropical frog).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Amphibia; Batrachia; Anura; Neobatrachia; Hyloidea; Leptodactylidae;  
 OC Leptodactylinae; Physalaemus.  
 OX NCBI\_TaxID=8378;  
 RN [1]  
 RP SEQUENCE.  
 RC TISSUE=Skin secretion;  
 RX MEDLINE=66076612; PubMed=5857249;  
 RA Erspamer V., Anastasi A., Bertaccini G., Cei J.M.;  
 RT "Structure and pharmacological actions of physalaemin, the main  
 RT active polypeptide of the skin of Physalaemus fuscumaculatus.";  
 RL Experientia 20:489-490(1964).  
 CC -!- FUNCTION: Tachykinins are active peptides which excite neurons,  
 CC evoke behavioral responses, are potent vasodilators and  
 CC secretagogues, and contract (directly or indirectly) many smooth  
 CC muscles.  
 CC -!- SUBCELLULAR LOCATION: Secreted.  
 CC -!- TISSUE SPECIFICITY: Skin.  
 CC -!- SIMILARITY: Belongs to the tachykinin family.  
 DR PIR; S07201; S07201.  
 DR InterPro; IPR002040; Tachy\_Neurokinin.  
 DR Pfam; PF02202; Tachykinin; 1.  
 DR PROSITE; PS00267; TACHYKININ; 1.  
 KW Amphibian defense peptide; Tachykinin; Neuropeptide; Amidation;  
 KW Pyrrolidone carboxylic acid.  
 FT MOD\_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.  
 FT MOD\_RES 11 11 AMIDATION.  
 SQ SEQUENCE 11 AA; 1283 MW; 3293693E59C33457 CRC64;

Query Match 9.1%; Score 1; DB 1; Length 11;  
 Best Local Similarity 100.0%; Pred. No. 9.8e+04;  
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 A 1  
 |  
 Db 2 A 2

# RESULT 69

## UF05\_MOUSE

ID UF05\_MOUSE STANDARD; PRT; 11 AA.  
 AC P38643;  
 DT 01-OCT-1994 (Rel. 30, Created)  
 DT 01-OCT-1994 (Rel. 30, Last sequence update)  
 DT 15-MAR-2004 (Rel. 43, Last annotation update)  
 DE Unknown protein from 2D-page of fibroblasts (P48) (Fragment).  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]

RP SEQUENCE.  
 RC TISSUE=Fibroblast;  
 RX MEDLINE=95009907; PubMed=7523108;  
 RA Merrick B.A., Patterson R.M., Wichter L.L., He C., Selkirk J.K.;  
 RT "Separation and sequencing of familiar and novel murine proteins  
 using preparative two-dimensional gel electrophoresis.";  
 RL Electrophoresis 15:735-745(1994).  
 CC -!- MISCELLANEOUS: On the 2D-gel the determined pI of this unknown  
 CC protein is: 5.5, its MW is: 48 kDa.  
 FT NON TER 11 11  
 SQ SEQUENCE 11 AA; 1328 MW; E54835E5CAAABAFA CRC64;

Query Match 9.1%; Score 1; DB 1; Length 11;  
 Best Local Similarity 100.0%; Pred. No. 9.8e+04;  
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 K 3  
 |  
 Db 1 K 1

# RESULT 70

## ULAG\_HUMAN

ID ULAG\_HUMAN STANDARD; PRT; 11 AA.  
 AC P31933;  
 DT 01-JUL-1993 (Rel. 26, Created)  
 DT 01-JUL-1993 (Rel. 26, Last sequence update)  
 DT 15-MAR-2004 (Rel. 43, Last annotation update)  
 DE Unknown protein from 2D-page of liver tissue (Spot 118) (Fragment).  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE.  
 RC TISSUE=Liver;  
 RX MEDLINE=94147969; PubMed=8313870;  
 RA Hughes G.J., Frutiger S., Paquet N., Pasquali C., Sanchez J.-C.,  
 RA Tissot J.-D., Bairoch A., Appel R.D., Hochstrasser D.F.;  
 RT "Human liver protein map: update 1993.";  
 RL Electrophoresis 14:1216-1222(1993).  
 CC -!- MISCELLANEOUS: On the 2D-gel the determined pI of this unknown  
 CC protein is: 5.5, its MW is: 34 kDa.  
 DR SWISS-2DPAGE; P31933; HUMAN.  
 DR Siena-2DPAGE; P31933; -.  
 FT NON TER 11 11  
 SQ SEQUENCE 11 AA; 1219 MW; EDABD37F272DDB0A CRC64;

Query Match 9.1%; Score 1; DB 1; Length 11;  
 Best Local Similarity 100.0%; Pred. No. 9.8e+04;  
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 A 1  
 |  
 Db 6 A 6

Search completed: April 8, 2004, 15:47:24  
Job time : 5.15385 secs